

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2004, 15:28:48 ; Search time 54 Seconds
(without alignments)
1292.393 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVIVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
1	1268	100.0	247	2	AAR84522	Aar84522 Stannioca
2	1268	100.0	247	3	AAB23264	Aab23264 Human sta
3	1268	100.0	247	3	AAY55750	Aay55750 Human sta
4	1268	100.0	247	3	AAY57166	Aay57166 Human cor
5	1268	100.0	247	3	AAY92901	Aay92901 Human sta
6	1268	100.0	247	4	AAB62473	Aab62473 Human sta
7	1268	100.0	247	4	AAB62690	Aab62690 Lng108, a
8	1268	100.0	247	5	ABB06259	Abb06259 Human sta
9	1268	100.0	247	6	ABP97748	Abp97748 Amino aci

10	1268	100.0	247	6	ABR47600	Abr47600 Breast ca
11	1268	100.0	247	6	ABG72290	Abg72290 Human Cor
12	1268	100.0	247	7	ADD48082	Add48082 Human Pro
13	1231	97.1	247	7	ADD48080	Add48080 Rat Prote
14	937	73.9	276	3	AAB56848	Aab56848 Human pro
15	680.5	53.7	261	1	AAP82968	Aap82968 Corpuscle
16	662.5	52.2	256	4	AAB62474	Aab62474 Coho salm
17	628	49.5	170	3	AAY55749	Aay55749 A. austra
18	358	28.2	70	4	AAM18134	Aam18134 Peptide #
19	358	28.2	70	4	ABB37166	Abb37166 Peptide #
20	358	28.2	70	4	AAM30637	Aam30637 Peptide #
21	358	28.2	70	4	ABB31928	Abb31928 Peptide #
22	358	28.2	70	4	ABB22472	Abb22472 Protein #
23	358	28.2	70	4	AAM70300	Aam70300 Human bon
24	358	28.2	70	4	AAM57878	Aam57878 Human bra
25	358	28.2	70	4	ABG52000	Abg52000 Human liv
26	358	28.2	70	4	AAM05763	Aam05763 Peptide #
27	358	28.2	70	5	ABG39940	Abg39940 Human pep
28	354.5	28.0	296	3	AAY67926	Aay67926 Mouse sta
29	354.5	28.0	296	4	AAB61623	Aab61623 Murine st
30	354	27.9	293	2	AAY41255	Aay41255 Adipogene
31	354	27.9	293	3	AAB26872	Aab26872 Human adi
32	354	27.9	293	4	AAB93965	Aab93965 Human pro
33	354	27.9	302	3	AAY67925	Aay67925 Human sta
34	354	27.9	302	4	AAB98971	Aab98971 Human adi
35	354	27.9	302	4	AAB61621	Aab61621 Human sta
36	354	27.9	302	4	AAB31797	Aab31797 Amino aci
37	354	27.9	302	4	AAB95330	Aab95330 Human pro
38	354	27.9	302	5	ABJ05546	Abj05546 Breast ca
39	354	27.9	302	5	AAE26113	Aae26113 Human BS2
40	354	27.9	302	6	ABR47601	Abr47601 Breast ca
41	354	27.9	302	6	ADA00844	Ada00844 Human bre
42	354	27.9	302	7	ADA27593	Ada27593 Human sta
43	354	27.9	302	7	ADB80516	Adb80516 Ovarian c
44	351.5	27.7	251	5	ABG32549	Abg32549 Human sta
45	346.5	27.3	301	6	ABU56615	Abu56615 Lung canc

ALIGNMENTS

RESULT 1

AAR84522

ID AAR84522 standard; protein; 247 AA.

XX

AC AAR84522;

XX

DT 19-APR-1996 (first entry)

XX

DE Stanniocalcin from Corpuscles of Stannius.

XX

KW stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;
KW electrolyte disorder; osteoporosis; Paget's disease; treatment.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .33
FT /label= prepro_region
FT Protein 34. .247
FT /label= mature_stanniocalcin
XX
PN WO9524411-A1.
XX
PD 14-SEP-1995.
XX
PF 09-MAY-1994; 94WO-US005136.
XX
PR 08-MAR-1994; 94US-00208005.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Olsen H, Adams MD;
XX
DR WPI; 1995-328227/42.
DR N-PSDB; AAT02438.
XX
PT Human corpuscles of Stannius polypeptide(s) - used to treat
PT hypercalcaemia, hypocalcaemia and other electrolyte disorders.
XX
PS Claim 14; Fig 1; 41pp; English.
XX
CC Stanniocalcin, a Corpuscles of Stannius polypeptide is encoded by
CC AAT02438. Stanniocalcin functions as a hypocalcaemic agent, and can be
CC used for the treatment of e.g. electrolyte disorders which lead to renal,
CC bone and heart diseases, hypertension, hypercalcaemia and disorders due
CC to elevated bone resorption, e.g. osteoporosis and Paget's disease
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 2
AAB23264
ID AAB23264 standard; protein; 247 AA.
XX
AC AAB23264;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human stanniocalcin.
XX
KW Human; stanniocalcin; STC; osteogenesis; bone disease; osteoporosis;
KW mineral metabolism regulator; prophylaxis; therapy.
XX
OS Homo sapiens.
XX
PN JP2000229880-A.
XX
PD 22-AUG-2000.
XX
PF 10-FEB-1999; 99JP-00033262.
XX
PR 10-FEB-1999; 99JP-00033262.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
DR WPI; 2000-605236/58.
DR N-PSDB; AAA97594.
XX
PT An osteogenesis promotor useful in the prevention and/or treatment of
PT bone diseases such as osteoporosis.
XX
PS Example 1; Page 5-6; 6pp; Japanese.
XX
CC The invention relates to a novel osteogenesis-promoting composition which
CC contains stanniocalcin (STC) as the active component. Stanniocalcin is a
CC possible regulator of mineral metabolism. The composition is useful as a
CC prophylactic and/or therapeutic agent for bone diseases such as
CC osteoporosis. The present sequence represents human stanniocalcin which
CC was used in an exemplification of the invention
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60
Db |||||||
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180
Db |||||||

Db 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
|||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
|||
Qy 241 RTSHESA 247
|||
Db 241 RTSHESA 247

RESULT 3

AAY55750

ID AAY55750 standard; protein; 247 AA.

XX

AC AAY55750;

XX

DT 11-FEB-2000 (first entry)

XX

DE Human stanniocalcin polypeptide.

XX

KW Stanniocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;
KW anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;
KW parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;
KW electrolyte disorder; renal; heart disease; osteopetrosis; human;
KW Paget's disease; hypercalcemia.

XX

OS Homo sapiens.

XX

PN US5994103-A.

XX

PD 30-NOV-1999.

XX

PF 02-JUN-1995; 95US-00460529.

XX

PR 10-NOV-1994; 94WO-US013206.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Fleischmann RD, Olsen HS;

XX

DR WPI; 2000-038260/03.

XX

PT Isolated nucleic acids encoding human stanniocalcin-alpha useful for
PT treating electrolyte disorders which lead to renal, bone and heart
PT diseases, osteoporosis and Paget's disease.

XX

PS Disclosure; Fig 3; 21pp; English.

XX

CC The invention provides a human stanniocalcin-alpha polypeptide (also
CC called teleocalcin and hypocalcin). Stanniocalcin-alpha is an anti-
CC hypercalcemic glycoprotein hormone produced by the corpuscles of
CC stannius. It has a similar reported biological activity to that of
CC parathyroid hormone (PTH) and both these proteins exhibit dual functions
CC in mammals. They exert hypercalcemic activity due to stimulation of bone
CC reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.
CC at low doses it increases bone formation and at high doses it increases

CC bone reabsorption. Accordingly, human stanniocalcin-alpha and antagonists
CC of it (under different circumstances) may be used to treat osteoporosis.
CC The DNA may be used to produce human stanniocalcin-alpha according to
CC standard recombinant DNA methodologies. The human stanniocalcin-alpha may
CC be produced either in vitro in a fermentation culture or in vivo as part
CC of a gene therapy protocol, and may be used to treat electrolyte
CC disorders which lead to renal, bone and heart diseases. Due to the
CC biphasic nature of stanniocalcin-alpha it may be used to treat
CC osteoporosis, osteopetrosis and Paget's disease. Alternatively, the
CC polypeptides may be used as antigens in the production of antibodies to
CC stanniocalcin-alpha and to assay for agonists and antagonists of its
CC activity. The antibodies and antagonists may be used to inhibit the
CC activity of stanniocalcin-alpha and may be used to treat osteoporosis and
CC hypercalcemia. The present sequence represents a human stanniocalcin

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240

Qy 241 RTSHESA 247
||| |||
Db 241 RTSHESA 247

RESULT 4

AAY57166

ID AAY57166 standard; protein; 247 AA.

XX

AC AAY57166;

XX

DT 11-FEB-2000 (first entry)

XX

DE Human corpuscles of stanius polypeptide.

XX

KW Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;
KW therapeutic; bone; heart disease; hypocalcemia; osteoperosis.

XX

OS Homo sapiens.

XX

PN US5994301-A.
XX
PD 30-NOV-1999.
XX
PF 28-APR-1995; 95US-00431117.
XX
PR 08-MAR-1994; 94US-00208005.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Adams MD, Olsen HS;
XX
DR WPI; 2000-038269/03.
DR N-PSDB; AAZ39520.
XX
PT Human corpuscles of stanius polypeptides used to inhibit calcium uptake.
XX
PS Claim 4; Fig 1A-B; 23pp; English.
XX
CC This represents a human corpuscles of stanius polypeptide, having a
CC calcium uptake inhibitory activity. The cDNA is deposited under the
CC accession number ATCC Deposit No. 75652. The polypeptide can be used in a
CC method for the treatment of a patient having need to inhibit uptake of
CC calcium. The method is also used for the therapeutic treatment of renal,
CC bone, and heart diseases, and the antagonist (may be an antibody) may be
CC used for treating hypocalcemia., and osteoperosis
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240

Qy 241 RTSHESA 247
||| |||
Db 241 RTSHESA 247

RESULT 5
AAV92901
ID AAV92901 standard; protein; 247 AA.

XX
AC AAY92901;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human stanniocalcin protein.
XX
KW PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
KW adipocyte; obesity; diabetes; hypertension; heart disease.
XX
OS Homo sapiens.
XX
PN WO200016795-A1.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-JP005080.
XX
PR 17-SEP-1998; 98JP-00263004.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
PI Goto M, Tomoyasu A, Yamaguchi K, Kinosaki M, Nakagawa N;
XX
DR WPI; 2000-283445/24.
DR N-PSDB; AAA11145.
XX
PT Treating or preventing obesity, which is a risk factor for diabetes,
PT hypertension and heart disease, comprises administering an agent
PT containing stanniocalcin.
XX
PS Example 1; Page 16; 19pp; Japanese.
XX
CC This sequence represents the human stanniocalcin protein. Stanniocalcin
CC is an inhibitor of the differentiation and maturation of adipocytes. The
CC protein is used for preventing and treating obesity which is a risk
CC factor for diabetes, hypertension, and heart disease. The coding sequence
CC was isolated from IMR-90 cells
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLN SALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLN SALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVC SIAKRNP EAITEVVQLPNHFSN RYYNRLVRS LLECD EDTVSTIRD 180
Db 121 IAEVQEECYSKLNVC SIAKRNP EAITEVVQLPNHFSN RYYNRLVRS LLECD EDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
||| |||
Db 241 RTSHESA 247

RESULT 6
AAB62473
ID AAB62473 standard; protein; 247 AA.
XX
AC AAB62473;
XX
DT 09-JUL-2001 (first entry)
XX
DE Human stanniocalcin (STC) protein.
XX
KW Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;
KW antirheumatic; antiarthritic; dermatological; antiallergic; human;
KW nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;
KW antiasthmatic; hemostatic; antiarrhythmic; vasotropic; antipsoriatic;
KW antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
KW hemostatic; thrombolytic.
XX
OS Homo sapiens.
XX
PN WO200130969-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US029432.
XX
PR 27-OCT-1999; 99US-0161740P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYHE-) UNIV HELSINKI.
XX
PI Olsen HS, Zhang K, Lindsberg P, Tatlisumak T, Kaste M;
PI Andersson LC;
XX
DR WPI; 2001-308626/32.
DR N-PSDB; AAF83297.
XX
PT Novel composition useful for treating or protecting neural cells, for
PT treating Addison's disease, organ rejection, hyperproliferative disorder,
PT cancer, AIDS, multiple sclerosis, comprises stanniocalcin polypeptide.
XX
PS Claim 1; Fig 1A-C; 253pp; English.
XX
CC The invention relates to a human stanniocalcin (STC) polypeptide. A
CC pharmaceutical composition comprising the STC is useful for treating a
CC patient in need of increased levels of STC activity. STC and its
CC modulators are useful for treating disorders or abnormalities of nervous
CC system, cerebrovascular diseases, dementia, encephalitis, central nervous
CC system infections or neoplasms, demyelinating diseases,

CC encephalomyelitis, spinal cord diseases, mental retardation such as
CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC reactions and conditions such as asthma, for treating and/or preventing
CC organ rejection or graft-versus-host disease, hyperproliferative diseases
CC such as purpura, Gaucher's disease, cardiovascular disorders such as
CC arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC disorders with neovascularization. The composition can be used to treat
CC hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed
CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC or detecting infectious agents. The present sequence represents the human
CC STC polypeptide
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSALQVGCGAFACL 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
||| |||
Db 241 RTSHESA 247

RESULT 7

AAB62690

ID AAB62690 standard; protein; 247 AA.

XX

AC AAB62690;

XX

DT 06-AUG-2001 (first entry)

XX

DE Lng108, a diagnostic marker for cancer.

XX

KW Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.

XX
OS Homo sapiens.
XX
PN WO200132209-A1.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-US030482.
XX
PR 04-NOV-1999; 99US-0163444P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Recipon H, Macina RA, Chen S, Sun Y;
XX
DR WPI; 2001-316386/33.
DR N-PSDB; AAF83823.
XX
PT Novel assay for diagnosing and monitoring cancer, involves determining levels of Lng108 in cells, tissues or bodily fluids of the patient, and comparing with control.
XX
PS Disclosure; Page 33-34; 36pp; English.
XX
CC The invention relates to diagnosing the presence of cancer or diagnosing metastases of cancer in a patient that involves determining levels of Lng108 in a sample of cells, tissues or bodily fluids in a patient, and comparing the determined levels with levels of Lng108 a normal human control. The method is useful for diagnosing the presence of cancer, diagnosing metastases of cancer, staging cancer, monitoring cancer, and monitoring a change in stage of the cancer, in a patient. A therapeutic agent which is an antibody labeled with paramagnetic ions or a radioisotope, and conjugated with a cytotoxic agent is useful for imaging cancer in a patient. A molecule which downregulates the expression or activity of Lng108, is useful for treating cancer in a patient. Lng108 protein is useful for inducing an immune response against a target cell expressing Lng108. The present sequence represents the human Lng108 polypeptide
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAACL 60
|||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
|||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCΣIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180
|||
Db 121 IAEVQEECYSKLNVCΣIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240

Qy 241 RTSHESA 247
||| |||
Db 241 RTSHESA 247

RESULT 8
ABB06259
ID ABB06259 standard; protein; 247 AA.
XX
AC ABB06259;
XX
DT 23-MAY-2002 (first entry)
XX
DE Human staniocalcin 1 protein.
XX
KW Human; staniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
KW rheumatic bone disease; cancer associated bone disease; rachitis;
KW arthritis deformans.
XX
OS Homo sapiens.
XX
PN WO200204013-A1.
XX
PD 17-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-JP005962.
XX
PR 11-JUL-2000; 2000JP-00209926.
XX
PA (BMLB-) BML INC.
XX
PI Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JE;
XX
DR WPI; 2002-164600/21.
DR N-PSDB; ABL40225.
XX
PT Agent used for treating bone diseases e.g. osteoporosis, traumatic bone
PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated
PT with cancer and arthritis deformans containing staniocalcin I.
XX
PS Claim 2; Fig 1; 24pp; Japanese.
XX
CC The present invention describes an agent containing staniocalcin 1,
CC particularly of human origin. Staniocalcin 1 has osteopathic activity.
CC The agent can be used for treating diseases relating to osteogenesis
CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone
CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated
CC with cancer, bone diseases due to phosphorus or calcium metabolic error,
CC rachitis and arthritis deformans. The agent increases bone mass. The
CC present sequence represents human staniocalcin 1
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 5; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.2e-123;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSALQVGCGAFACL 60
Db	1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSALQVGCGAFACL 60
Qy	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Qy	121 IAEVQEECYSKLNVCSTIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
Db	121 IAEVQEECYSKLNVCSTIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
Qy	181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db	181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Qy	241 RTSHESA 247
Db	241 RTSHESA 247

RESULT 9
 ABP97748
 ID ABP97748 standard; protein; 247 AA.
 XX
 AC ABP97748;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Amino acid sequence of human STC1 polypeptide.
 XX
 KW Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;
 KW microvasculopathy; bone healing; skin inflammation; HOG3; HOG8; HOG18;
 KW follicular development; CA9; HXB; IGFBP5; HFARP; STC1; mig-6; SSR4;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2003010205-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 26-JUL-2002; 2002WO-US023786.
 XX
 PR 26-JUL-2001; 2001US-0307600P.
 PR 24-JUL-2002; 2002US-00201642.
 XX
 PA (UYDU-) UNIV DUKE MEDICAL CENT.
 XX
 PI Riggins GJ, Lal A;
 XX
 DR WPI; 2003-239423/23.

DR N-PSDB; ABZ77288.

XX

PT Inhibiting angiogenesis for treating wound healing, retinopathy,
PT ischemia, inflammation, microvasculopathy, bone healing, skin
PT inflammation or follicular development by providing to a subject an
PT antisense polynucleotide.

XX

PS Claim 4; Page 61; 66pp; English.

XX

CC The present sequence is a human STC1 polypeptide. It is used in the
CC method of the invention. The specification describes a method modulating
CC angiogenesis associated with wound healing, retinopathy, ischemia,
CC inflammation, microvasculopathy, bone healing, skin inflammation or
CC follicular development. The method comprises providing to a subject HOG3,
CC HOG8, HOG18, CA9, HXB, IGFBP5, HFARP, STC1, mig-6 or SSR4. The methods,
CC antisense polynucleotides, polypeptides and antibodies are useful for
CC treating wound healing, retinopathy, ischemia, inflammation,
CC microvasculopathy, bone healing, skin inflammation or follicular
CC development, or cancer such as breast, colon or lung cancer, or
CC glioblastoma

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRLNSALQVGCGAFACL 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHIQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 SLMEKIGPNMASLFHIQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
||||||

Db 241 RTSHESA 247

RESULT 10

ABR47600

ID ABR47600 standard; protein; 247 AA.

XX

AC ABR47600;

XX

DT 12-JUN-2003 (first entry)

XX

DE Breast cancer associated protein sequence SEQ ID NO:441.

XX
KW Human; breast cancer; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003004989-A2.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019669.
XX
PR 21-JUN-2001; 2001US-0299887P.
PR 27-JUN-2001; 2001US-0301572P.
PR 18-JUL-2001; 2001US-0306501P.
PR 25-SEP-2001; 2001US-0325002P.
PR 05-MAR-2002; 2002US-0362585P.
PR 14-MAY-2002; 2002US-0380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
XX
DR WPI; 2003-210381/20.
DR N-PSDB; ACC50301.
XX
PT Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
PS Claim 1; SEQ ID NO 441; 128pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQN SAEVVCLNSALQVGCGAACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQN SAEVVCLNSALQVGCGAACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
|||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCSTI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
|||
Db 121 IAEVQEECYSKLNVCSTI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240
|||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240

Qy 241 RTSHESA 247
|||
Db 241 RTSHESA 247

RESULT 11

ABG72290

ID ABG72290 standard; protein; 247 AA.

XX

AC ABG72290;

XX

DT 14-MAR-2003 (first entry)

XX

DE Human Corpuscles of Stannius protein.

XX

KW Human; Corpuscles of Stannius protein; calcium uptake inhibitor;
KW renal excretion of phosphate; electrolyte disorder; renal disease;
KW bone disease; heart disease; arterial hypertension; bone resorption;
KW osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;
KW hypervitaminosis D; tumour; serum calcium level; sarcoidosis;
KW hyperthyroidism; adrenal insufficiency; serum albumin; plasma protein;
KW GI calcium absorption; stanniocalcin; osteopathic; cytostatic;
KW hypotensive.

XX

OS Homo sapiens.

XX

PN US2002146791-A1.

XX

PD 10-OCT-2002.

XX

PF 05-APR-2002; 2002US-00116051.

XX

PR 08-MAR-1994; 94US-00208005.

PR 28-APR-1995; 95US-00431117.

PR 17-MAY-1999; 99US-00312610.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Olsen HS, Adams MD;

XX

DR WPI; 2003-147579/14.

DR N-PSDB; ABX15152.

XX

PT Isolated polynucleotide for encoding polypeptides used to diagnose and
PT treat electrolyte disorders leading to renal disease, e.g. Paget's

PT disease, hypercalcemia and sarcoidosis.
XX
PS Claim 13; Fig 1; 26pp; English.
XX
CC The present invention relates to the isolation of human Corpuscles of
CC Stannius protein, and the polynucleotide sequence encoding it. Human
CC Corpuscles of Stannius protein inhibits calcium uptake and reduces renal
CC excretion of phosphate. The polynucleotide sequence is useful for
CC encoding Corpuscles of Stannius protein for therapeutic purposes, e.g. in
CC the treatment of electrolyte disorders that lead to renal, bone or heart
CC disease, such as arterial hypertension, disorders due to elevated bone
CC resorption (e.g. osteoporosis and Paget's disease), and hypercalcaemia
CC (e.g. hyperparathyroidism, hypervitaminosis D), tumours that raise serum
CC calcium levels by destroying bone, sarcoidosis, hyperthyroidism, adrenal
CC insufficiency, loss of serum albumin secondary to renal diseases, or
CC excessive GI calcium absorption and elevated concentration of plasma
CC proteins. The encoded polypeptide exhibits a high degree of homology to
CC Stanniocalcin from Anguilla australis and from Oncorhynchus kisutch. The
CC present sequence represents human corpuscles of stannius protein
XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCILNSALQVGCGAFACL 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCILNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
||| |||
Db 241 RTSHESA 247

RESULT 12
ADD48082
ID ADD48082 standard; protein; 247 AA.
XX
AC ADD48082;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P52823, SEQ ID NO 13779.
XX

KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P52823.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLECDDETVSTIRD 180
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLECDDETVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 13

ADD48080

ID ADD48080 standard; protein; 247 AA.

XX

AC ADD48080;

XX

DT 29-JAN-2004 (first entry)

XX

DE Rat Protein P97574, SEQ ID NO 13777.

XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX

OS Rattus norvegicus.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; P97574.

XX

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 247 AA;

Query Match 97.1%; Score 1231; DB 7; Length 247;
Best Local Similarity 96.0%; Pred. No. 8.6e-120;
Matches 237; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60
||| ||| :| | ||| :| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MLQNSA VILALVISAAAHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||| ||| :| | ||| ||| ||| ||| :| | ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQE E CYS KLN VCSIAKR NPE AITE VVQLPNHFSNRYYRN LVR SLL ECDED TVSTIRD 180
||| ||| :| | ||| ||| ||| ||| ||| :| | ||| ||| ||| ||| ||| ||| |||
Db 121 IAEVQE D CYS KLN VCSIAKR NPE AITE VIQLPNHFSNRYYRN LVR SLL ECDED TVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEGDSPSHIK 240

Qy 241 RTSHESA 247
||| :|
Db 241 RTSQENA 247

RESULT 14
AAB56848
ID AAB56848 standard; protein; 276 AA.
XX
AC AAB56848;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1426.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005988.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
DR N-PSDB; AAF16051.
XX
PT Prostate cancer associated gene sequences, referred to as prostate cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as prostate cancer.
XX
PS Claim 11; Page 1858-1859; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,

CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention

XX

SQ Sequence 276 AA;

Query Match 73.9%; Score 937; DB 3; Length 276;
Best Local Similarity 99.5%; Pred. No. 5e-89;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCILNSALQVGCGAFACL 60
Db 89 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCILNSALQVGCGAFACL 148

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 149 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 208

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180
Db 209 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 268

Qy 181 SLMEKI 186
Db 269 SLMEXI 274

RESULT 15

AAP82968

ID AAP82968 standard; protein; 261 AA.

XX

AC AAP82968;

XX

DT 25-MAR-2003 (revised)

DT 30-NOV-1990 (first entry).

XX

DE Corpuscles of Stannius CS protein precursor.

XX

KW Corpuscles of Stannius; CS protein; cardiovascular disease; oedema;

KW heart failure; high blood pressure.

XX

OS Anguilla australis.

XX

FH Key Location/Qualifiers

FT Peptide 1. .17

FT /label= signal peptide/prohormone

FT Peptide 18. .288

FT /label= pro-CS

XX

PN WO8803949-A.

XX

PD 02-JUN-1988.

XX

PF 19-NOV-1987; 87WO-AU000389.

XX

PR 21-NOV-1986; 86AU-00009107.

PR 31-DEC-1986; 87AU-00082797.
PR 22-MAY-1987; 87AU-00002086.
XX
PA (FLOR-) FLOREY INST EXPER.
PA (BUTK/) BUTKUS A.
XX
PI Butkus A, Coghlan JP, Roche PJ;
XX
DR WPI; 1988-161619/23.
DR N-PSDB; AAN80655.
XX
PT CS protein of corpuscles of stannius - used for treating cardiovascular disease, renal disease and electrolyte disorders.
XX
PS Disclosure; Page ?; 38pp; English.
XX
CC This prepro-CS protein sequence has its signal or pro-hormone fragment (amino acids -17 to 1) cleaved to yield the pro-CS form which can be processed to yield the mature form. Recombinant DNA methods are utilised in the prodn. of the CS protein. It is useful as e.g. a therapeutic agent for the treatment of cardiovascular disease and oedema. See also AAN80654. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 261 AA;

Query Match 53.7%; Score 680.5; DB 1; Length 261;
Best Local Similarity 61.4%; Pred. No. 2.8e-62;
Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;

Qy 1 MLQNSAVLLVLVISA\$ATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60
||: | ::| ||: :| :| :::: :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 1 MLRMSGGLILTLVL-VTAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFAACL 59

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
:||||:||||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 60 DNSTCNDGMHEICRSFLHGAAKFDTQGKTFVKEALKCIANGITSKVFLTIRCSSFQKM 119

Qy 121 IAEVQEECYSKLNVCSTIAKRNPAAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180
|:||||||||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 120 ISEVQEECYSKLDLCSVQAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLLTCDDEDTVQEVR 179

Qy 181 SLMEEKIGPNMASLFHILQTDHC 202
|: ::| | | || :||| |
Db 180 GLVSRLEPEMGVLFQLLQTKAC 201

Search completed: July 19, 2004, 15:32:16
Job time : 57 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2004, 15:31:13 ; Search time 19 Seconds
(without alignments)
671.138 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	247	2 US-08-208-005C-2	Sequence 2, Appli
2	1268	100.0	247	2 US-09-038-597A-2	Sequence 2, Appli
3	1268	100.0	247	2 US-08-460-529B-10	Sequence 10, Appl
4	1268	100.0	247	2 US-08-431-117A-2	Sequence 2, Appli
5	1268	100.0	247	4 US-09-361-736B-10	Sequence 10, Appl
6	660.5	52.1	204	2 US-08-208-005C-5	Sequence 5, Appli
7	660.5	52.1	204	2 US-09-038-597A-5	Sequence 5, Appli
8	628	49.5	170	2 US-08-460-529B-9	Sequence 9, Appli
9	628	49.5	170	4 US-09-361-736B-9	Sequence 9, Appli
10	354.5	28.0	296	3 US-08-831-132-14	Sequence 14, Appli
11	354.5	28.0	296	3 US-09-416-150-14	Sequence 14, Appli

12	354	27.9	302	3	US-08-831-132-2	Sequence 2, Appli
13	354	27.9	302	3	US-09-416-150-2	Sequence 2, Appli
14	354	27.9	302	4	US-09-193-881-23	Sequence 23, Appl
15	354	27.9	302	4	US-09-361-736B-12	Sequence 12, Appl
16	351.5	27.7	251	4	US-09-361-736B-2	Sequence 2, Appli
17	333.5	26.3	251	2	US-08-460-529B-2	Sequence 2, Appli
18	89.5	7.1	10182	4	US-09-134-001C-3159	Sequence 3159, Ap
19	86	6.8	500	4	US-09-198-452A-299	Sequence 299, App
20	85.5	6.7	656	4	US-09-134-001C-4322	Sequence 4322, Ap
21	83.5	6.6	290	4	US-09-655-908-6	Sequence 6, Appli
22	83.5	6.6	290	4	US-09-655-908-8	Sequence 8, Appli
23	83.5	6.6	1027	4	US-09-762-724-8	Sequence 8, Appli
24	83.5	6.6	1029	4	US-09-762-724-6	Sequence 6, Appli
25	83	6.5	417	4	US-09-134-001C-3810	Sequence 3810, Ap
26	82	6.5	362	4	US-09-134-001C-4670	Sequence 4670, Ap
27	81	6.4	680	4	US-09-298-924-4	Sequence 4, Appli
28	81	6.4	720	2	US-08-840-236-1	Sequence 1, Appli
29	81	6.4	720	2	US-08-505-448A-1	Sequence 1, Appli
30	79.5	6.3	708	1	US-08-145-681-4	Sequence 4, Appli
31	79.5	6.3	708	1	US-08-453-703-4	Sequence 4, Appli
32	79.5	6.3	708	2	US-08-456-106-4	Sequence 4, Appli
33	79.5	6.3	708	3	US-08-456-108-4	Sequence 4, Appli
34	79.5	6.3	708	3	US-09-265-577-4	Sequence 4, Appli
35	79.5	6.3	708	4	US-09-633-739-4	Sequence 4, Appli
36	79	6.2	264	4	US-09-134-000C-5831	Sequence 5831, Ap
37	78.5	6.2	1288	4	US-09-546-934-4	Sequence 4, Appli
38	78	6.2	315	4	US-09-184-964-4	Sequence 4, Appli
39	78	6.2	338	4	US-09-328-352-4723	Sequence 4723, Ap
40	78	6.2	383	4	US-09-328-352-5969	Sequence 5969, Ap
41	78	6.2	781	4	US-09-738-946-8	Sequence 8, Appli
42	77.5	6.1	467	2	US-08-686-599A-17	Sequence 17, Appl
43	76.5	6.0	315	4	US-09-615-192A-378	Sequence 378, App
44	76	6.0	376	4	US-09-489-039A-10020	Sequence 10020, A
45	76	6.0	2802	3	US-09-542-331-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-208-005C-2

; Sequence 2, Application US/08208005C

; Patent No. 5837498

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN

US-08-208-005C-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.3e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 2
US-09-038-597A-2
; Sequence 2, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,597A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-038-597A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.3e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCI NSALQVGCGA FACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCI NSALQVGCGA FACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQE ECYSKLNVC SIAKRNP EAITEVVQLPNHFSN RYYNRLVRSLL ECDED TVSTIRD 180
Db 121 IAEVQE ECYSKLNVC SIAKRNP EAITEVVQLPNHFSN RYYNRLVRSLL ECDED TVSTIRD 180

Qy 181 SLMEKIGP NMASLFH ILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGP NMASLFH ILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAACL 60
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Qy 121 IAEVQEECYSKLNVCASIARKRNPEAITEVVQLPNHFSNRYYNRLVRSLLLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCASIARKRNPEAITEVVQLPNHFSNRYYNRLVRSLLLECDEDTVSTIRD 180
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 4

US-08-431-117A-2

; Sequence 2, Application US/08431117A
; Patent No. 5994301
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,117A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8 MARCH 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS

; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.3e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 5

US-09-361-736B-10

; Sequence 10, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.3e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60
|||
Db 1 MLQNSAVLLVLVISASATHEAEQNDVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
|||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
|||
Db 121 IAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
|||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
|||
Db 241 RTSHESA 247

RESULT 6

US-08-208-005C-5

; Sequence 5, Application US/08208005C

; Patent No. 5837498

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/208,005C

; FILING DATE: 8 MARCH 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-78

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 5:

; FILING DATE: 8-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-038-597A-5

Query Match 52.1%; Score 660.5; DB 2; Length 204;
Best Local Similarity 60.8%; Pred. No. 3.7e-67;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

Qy 11 LVISASATHEAEQNDSVSPRKSRAAQNAAEVVRCLNLSALQVGCGAFACLENSTCDTDGM 70
||: :|| : : :: |||:::| : : : ::| |||| | ||| | ||| | ||| | ||| | |||
Db 12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
:|||: | ::||| | :||| | ||| | :||| | ||| | :||| | ||| | :||| | |||
Db 71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFTIRRCGVFQRMISEVQEECYS 130

Qy 131 KLNVCSTIAKRNPAAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRDSLMEKIGPNM 190
:||:| :|: | |||| | |||:| | | |||: | :||| | |||:|:| | :| :|||:
Db 131 RLDICGVARSNPEAIGEVVQVPAHFNPRYYSTLLQSLLACDEETVAVVRAGLVARLGPD 190

Qy 191 ASLFHILQTDHCAQ 204
:|| :|| | | |
Db 191 ETLFQLLQNKHCPQ 204

RESULT 8

US-08-460-529B-9

; Sequence 9, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,529B
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13206
FILING DATE: 10 NOV 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN

RESULT 9

US-09-361-736B-9
; Sequence 9, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-09-361-736B-9

Query Match 49.5%; Score 628; DB 4; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.4e-63;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Qy 28 SPRKSRVAAQNSAEVVRLNSALQVGCGAFACILENSTCDTDGMYDICKSFLYSAAKFDTQ 87
||| :| :| : ::| ||||| ||||||| |||||:||||:||||:|||:|||: |||||||
Db 1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ 60

Qy 88 GKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCASIKNPEAITE 147
|| |||||||:||||| |||||:|||:|||:|||||:|||:|||:|||:
Db 61 GKTFVKESLKCIAANGITSKVFTIRRCSSFQKMISEVQEECYSKLDLCSVQAQSNEAMGE 120

Qy 148 VVQLPNHFSNRYYNRLVRSLLCDEDTVEQVRAGLVSLEPEMGVLFQLL 197
| |::| | |||: |::||| ||||| :| |: :: || | | :|
Db 121 VAQVPSQFPNRYYSTLLQSLTCDEDTVEQVRAGLVSLEPEMGVLFQLL 170

RESULT 10

US-08-831-132-14

; Sequence 14, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOLCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-416-150-14

Query Match 28.0%; Score 354.5; DB 3; Length 296;
Best Local Similarity 31.7%; Pred. No. 5.4e-32;
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

Qy 7 VLLVLVISASATHEAEQNDSVSP-----RKSRAAQNSAEVVRCLNSALQVGCGA 56
| | || : | : | : | : | : | : | : | : | : | : |
Db 10 VTLALVF--ATLDPAQGTDSTNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVCGV 67

Qy 57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCST 116
| | ||::|: |::| | :||::| | || | ||::|:| | : | | | :|
Db 68 FECFENNNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKGFCISRKCPA 127

Qy 117 FQRMIAEVQECCYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVS 176
: |: ::| | || | :|| | : | | | : | : | | || | ||
Db 128 IREMVFQLQRECYLKHDLCSAAQENVGVIVEMIFKDLLLHEPYVDLVNLLLTCGEDVKE 187

Qy 177 TIRDSEMEKIGPNMASLFHIL-----QTDHCAQTH---PRADFNRRRTNEPQKLKV 224
: |: : | | | : | : | | | : | | | : | : |
Db 188 AVTRSVQAQCEQSWGGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHRDTDHHLT 247

Qy 225 LLRNLRGEEDSPSHIK----RTSHESA 247
| :|| | || | :|| :||
Db 248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275

RESULT 12
US-08-831-132-2
; Sequence 2, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.

; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-831-132-2

Query Match 27.9%; Score 354; DB 3; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.4e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRSRVAQNSAEVVRCLNSALQVGCGAACL 60
| ||::: ||: | | | :| |:: ||:||: | | :| | ||| | |
Db 12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVCGVFECF 71

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||::|: |::|:| || ::|:| | || |::|:|:|:| |: | :| |:| :|
Db 72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALCKAHALRHRCISRKCPAIREM 131

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
:::| | || | :|:| |:| | | |::| :| | | | | |:| |
Db 132 VSQLQRECYLKHDLCAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLTCGEEVKEAITH 191

Qy 181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL----- 222
|: | :| | | | | | | | | |: | :| |
Db 192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTLSRAHHGEAGHHLPEPSS 251

Qy 223 KVLLRNLRGEEDSPSH 238

: | :|| |||
Db 252 RETGRGAKGERGSKSH 267

RESULT 13
US-09-416-150-2
; Sequence 2, Application US/09416150
; Patent No. 6171822
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; Conklin, Darrell C.
; Lok, Si
; Buddle, Michele
; Downey, William
; TITLE OF INVENTION: STANNIOLCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-416-150-2

Query Match 27.9%; Score 354; DB 3; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.4e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVTS-----ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLN SALQVGCGAFACL 60
| ||::: ||: | | | | :| | ::| ||:||: | | :| | ||| | |

Db 12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71
 Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKEALKCIANGVTSKVFLAIRRCSTFQRM 120
 ||::|: |:: || :||:| ||| |||:|:||:||| : : : |:| : |
 Db 72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIDALKCKAHALRHRFGCISRKCPCAIREM 131
 Qy 121 IAEVQEECYSKLNVCASIARKRNPEAITEEVVQLPNHFSNRYNRLLVRSLLECDEDTVSTIRD 180
 ::::| ||| | ::|:| :| | | |:: : : | ||| ||| |: |
 Db 132 VSQQLRECYLKHDLCAAAQENTRVIVEMIHFKDLLHEPYVDLVNLLTCGEEVKEAITH 191
 Qy 181 SLMEKIGPNMASLFIHQ-TDHCAQTHPRADFNRRRTNEPQKL----- 222
 |: : | | || | | | | | |: : |
 Db 192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251
 Qy 223 KVLLRNLRGEDSPSH 238
 : | :|| | |||
 Db 252 RETGRGAKGERGSKSH 267

RESULT 14

US-09-193-881-23

; Sequence 23, Application US/09193881A
 ; Patent No. 6538119
 ; GENERAL INFORMATION:
 ; APPLICANT: Patricia Billing-Medel
 ; APPLICANT: Maurice Cohen
 ; APPLICANT: Tracey L. Colpitts
 ; APPLICANT: Paula N. Friedman
 ; APPLICANT: Edward N. Granados
 ; APPLICANT: Michael R. Klass
 ; APPLICANT: John C. Russell
 ; APPLICANT: Stephen D. Stroupe
 ; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
 ; TITLE OF INVENTION: Breast
 ; FILE REFERENCE: 6248.US.P1
 ; CURRENT APPLICATION NUMBER: US/09/193,881A
 ; CURRENT FILING DATE: 1998-11-18
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 302
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-193-881-23

Query Match 27.9%; Score 354; DB 4; Length 302;
 Best Local Similarity 32.4%; Pred. No. 6.4e-32;
 Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60
 | ||::: | |: | | | :| |:: ||:||: | | :| | | | | |
 Db 12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71
 Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKEALKCIANGVTSKVFLAIRRCSTFQRM 120
 ||::|: |:: || :||:| ||| |||:|:||:||| : : : |:| : |
 Db 72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIDALKCKAHALRHRFGCISRKCPCAIREM 131

Db

252 RETGRGAKGERGSKSH 267

Search completed: July 19, 2004, 15:34:25

Job time : 20 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2004, 15:30:13 ; Search time 16 Seconds
(without alignments)
1484.957 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	680.5	53.7	263	2	A54648	stanniocalcin prec
2	662.5	52.2	256	2	I51197	stanniocalcin - co
3	354	27.9	302	2	JE0357	stanniocalcin homo
4	150	11.8	40	2	B60841	teleocalcin - coho
5	149	11.8	40	2	A60841	teleocalcin - sock
6	123	9.7	33	2	S06337	teleocalcin - rain
7	102	8.0	473	2	T04799	hypothetical prote
8	94	7.4	1105	2	T18295	Ap-3 adaptor compl
9	90.5	7.1	289	2	T50776	hypothetical prote
10	90.5	7.1	783	2	T38690	probable regulator
11	89.5	7.1	1126	2	T01491	ubiquitin-protein
12	89	7.0	305	2	T08121	peroxidase (EC 1.1
13	88	6.9	473	2	T45954	hypothetical prote

14	87.5	6.9	1465	2	S45628	DNA-directed DNA p
15	86	6.8	470	2	H72097	mg++ transporter (
16	86	6.8	470	2	F86526	Mg++ transporter [
17	86	6.8	510	2	T45952	hypothetical prote
18	86	6.8	556	2	S51858	probable membrane
19	86	6.8	581	2	S58201	probable membrane
20	83	6.5	250	2	S30584	hypothetical prote
21	83	6.5	250	2	D69215	conserved hypothet
22	83	6.5	365	2	T06693	hypothetical prote
23	83	6.5	1093	2	T50652	AP-3 complex beta3
24	83	6.5	1094	2	T50651	AP3-complex beta-3
25	82.5	6.5	869	2	A88710	protein C43G2.2 [i
26	82.5	6.5	1483	2	S30015	hypothetical prote
27	82.5	6.5	1757	2	T05204	hypothetical prote
28	82.5	6.5	2335	2	T40186	probable phosphati
29	82.5	6.5	2535	2	T04824	hypothetical prote
30	82	6.5	815	2	G72209	conserved hypothet
31	82	6.5	925	2	T01384	hypothetical prote
32	81.5	6.4	463	2	T15416	hypothetical prote
33	81.5	6.4	549	2	F64640	conserved hypothet
34	81.5	6.4	708	1	TFBOL	lactotransferrin p
35	81	6.4	358	2	S76692	hypothetical prote
36	81	6.4	720	2	JC5131	glycosyltransferas
37	81	6.4	1375	2	T18961	FAB1 protein homol
38	81	6.4	4377	2	A55575	ankyrin 3, long sp
39	80	6.3	281	2	H84720	probable endonucle
40	80	6.3	509	1	VGNVPC	major envelope gly
41	80	6.3	509	2	T10395	protein gp64 - Org
42	80	6.3	985	2	T00633	Ca2+-transporting
43	80	6.3	998	2	T52581	Ca2+-transporting
44	80	6.3	1178	2	S54073	probable membrane
45	80	6.3	1188	2	T46608	zinc finger protei

ALIGNMENTS

RESULT 1

A54648

stanniocalcin precursor - Australian eel

N;Alternate names: Stannius corpuscle secretory protein

C;Species: Anguilla australis (Australian eel)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C;Accession: A54648

R;Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.;

Ryan, G.B.; Trahair, J.F.; Tregear, G.W.; Coghlan, J.P.

Mol. Cell. Endocrinol. 54, 123-133, 1987

A;Title: Purification and cloning of a corpuscles of Stannius protein from
Anguilla australis.

A;Reference number: A54648; MUID:88083961; PMID:3319739

A;Accession: A54648

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-263 <BUT>

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-263/Product: stanniocalcin #status predicted <MAT>

Query Match 53.7%; Score 680.5; DB 2; Length 263;
 Best Local Similarity 61.4%; Pred. No. 2.3e-51;
 Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;

Qy	1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRRVAAQNSAEVVRLNSALQVGCGAFACL 60 : :: : : : :::: : : : : ::
Db	1 MLRMSGILTLVLT-VTAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFACL 59
Qy	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESSLKCIANGVTSKVFLAIRRCSTFQRM 120 : : : : : : : :
Db	60 DNSTCNDGMHEICRSFLHGAAKFDTQGKTFVKESSLKCIANGITSKVFLTIRRCSSFQKM 119
Qy	121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLLECDEDTVSTIRD 180 : : : : : : : : : :
Db	120 ISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRA 179
Qy	181 SLMEKIGPNMASLFHILQTDHC 202 : :: :
Db	180 GLVSRLPEPMGVLFQQLQTKAC 201

RESULT 2

I51197

stanniocalcin - coho salmon

C;Species: Oncorhynchus kisutch (coho salmon)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Accession: I51197

R;Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.

Mol. Cell. Endocrinol. 90, 7-15, 1992

A;Title: Molecular cloning and cDNA sequence analysis of coho salmon stanniocalcin.

A;Reference number: I51197; MUID:93246046; PMID:1363790

A;Accession: I51197

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-256 <WAG>

A;Cross-references: GB:S59519; NID:g299926; PIDN:AAB26419.1; PID:g299927

Query Match 52.2%; Score 662.5; DB 2; Length 256;
 Best Local Similarity 53.4%; Pred. No. 8.1e-50;
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

Qy	11 LVISASATHEAEQNDSVSPRKSRRVAAQNSAEVVRLNSALQVGCGAFACLENSTCDTDGM 70 : : : : :: : : : : :
Db	12 LVLGTAATFDTPPEA-SPRRARFSSNSPSDVARCLNGALAVCGTFACLENSTCDTDGM 70
Qy	71 YDICKSFLYSAAKFDTQGKAFVKESSLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130 : : : : : : :
Db	71 HDICQLFFHTAATFNTQGKTFVKESSLRCIANGVTSKVFTQTIIRRCGVFQRMISEVQEECYS 130
Qy	131 KLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLLECDEDTVSTIRDLSMEKIGPNM 190 : : : : : : : : : : : : :
Db	131 RLDICGVARSNPEAIGEVVQVPAHFNPNEYSTLLQSLACDEETVAVVRAGLVARLGPM 190
Qy	191 ASLFHILQTDHCAQTHPRADFN----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239 : : : : : : : : :
Db	191 ETLFQQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241

RESULT 3

JE0357

stanniocalcin homolog - human

N;Alternate names: STC2

C;Species: Homo sapiens (man)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000

C;Accession: JE0357

R;Ishibashi, K.; Miyamoto, K.; Taketani, Y.; Morita, K.; Takeda, E.; Sasaki, S.; Imai, M.

Biochem. Biophys. Res. Commun. 250, 252-258, 1998

A;Title: Molecular cloning of a second human stanniocalcin homologue (STC2).

A;Reference number: JE0357; MUID:98440784; PMID:9753616

A;Accession: JE0357

A;Molecule type: mRNA

A;Residues: 1-302 <ISH>

A;Cross-references: DDBJ:AB012664; NID:g3702223; PIDN:BAA33489.1; PID:g3702224

C;Comment: This protein suppressed expression of renal sodium/phosphate cotransporter.

C;Genetics:

A;Introns: 51/1 98/3 169/2

Query Match 27.9%; Score 354; DB 2; Length 302;
Best Local Similarity 32.4%; Pred. No. 4.6e-23;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKSRSVAAQNSAEVVRCILNSALQVGCGAFACL 60
| ||::: ||: | | | | : ||:: ||:: ||: || | | || | | | | | |

Db 12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||:::| |::| | :||::| | || | ||::|:||::| | :| :| | :| |

Db 72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALCKKAHALRHRFGCISRKCPAIREM 131

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYNRNLVRSLLECDEDTVSTIRD 180
::::| | || | ::|: |: | | | |::| :| | | | | | | | | | |

Db 132 VSQQLRECYLKHDLCAAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLTCGEEVKEAITH 191

Qy 181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL----- 222
|: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHLPEPSS 251

Qy 223 KVLLRNLRGEEDSPSH 238
: | :|| | ||

Db 252 RETGRGAKGERSKSH 267

RESULT 4

B60841

teleocalcin - coho salmon (fragment)

C;Species: Oncorhynchus kisutch (coho salmon)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993

C;Accession: B60841

R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.

Gen. Comp. Endocrinol. 72, 237-246, 1988

A;Title: Identification of hypocalcin (teleocalcin) isolated from trout stannius corpuscles.
A;Reference number: S06337; MUID:88196801; PMID:3360288
A;Accession: SQ6337
A;Molecule type: protein
A;Residues: 1-33 <LAF>
A;Note: 7-Glu was also found
C;Keywords: dimer; glycoprotein; hormone
F;29/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 9.7%; Score 123; DB 2; Length 33;
Best Local Similarity 65.6%; Pred. No. 0.00032;
Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy	35 AAQNSAEVVRCLNSALQVGCGAFACLENSTCD 66
	:: : ::
Pb	2 SSNSPSDVARCLNGALAVGCGTFACLENSTCD 33

RESULT 7

T04799

hypothetical protein F10M23.100 - *Arabidopsis thaliana*

C; Species: *Arabidopsis thaliana* (mouse-ear cress)

C; Date: 23-Apr-1999 #sequence revision 23-Apr-1999 #text change 11-Jun-1999

C;Accession: T04799

R; Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueler, C.

submitted to the Protein Sequence Database

A; Reference number: Z15385

A;Accession: T04799

A; Molecule type: DNA

A; Residues: 1-473 <BEV>

A;Cross-references: EMBL:AL035440

A; Experimental source: cultivar Columbia; BAC clone F10M23

C: Genetics:

A; Map position: 4

A; Introns: 24/3; 92/3; 184/3; 256/3; 308/3; 412/3

A; Note: F10M23, 100

Query Match 8.0%; Score 102; DB 2; Length 473;
Best Local Similarity 21.0%; Pred. No. 0.49;
Matches 50; Conservative 43; Mismatches 67; Indels 78; Gaps 11;

Qy 26 SVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDT----DGMYDICKSF-LYS 80
 :| :| :||:: ||::: |: | :| | | ||| | :|:
 Db 50 NVYKKKVELAAKSRAELLOTLS-----ATVELSNLTALGEKSYIDICDSMSLFP 100

Qy 81 AAKFDTQGKAFVKE~~SL~~KCIA-----NG-- 102
| | :|||

Pb 101 LOPDKTSGT--IKEOLSATAPALEOLWOKEERVRAFSDVOSOTOKICEELAGGLNNGP 158

Qy 103 VTSKVFLAIRRCSTFQRMIAEVQEECYSKL-----NVCSTIAKRN-PEAITEV-- 148

Pb 159 VVDETDLSLKRLDDFORKLOELOKEKSDRLOKVLEFVSTVHDLCAVLRLDELSTVTEVHP 218

Qy 149 -----VQLPNHFSRYYNRNLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQT 199

DB 219 SLDEANGVQTKS-INSNETLARLAKTVLTLKEDKMQLKK--LQELATQLTDLWNLMDT 273

RESULT 8

T18295

Ap-3 adaptor complex beta3A chain - mouse

C;Species: *Mus musculus* (house mouse)

C:\Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 15-Oct-1999

C:Accession: T18295

R; Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; Rusiniak, M.E.; Eicher, E.M.; Robinson, M.S.; Gorin, M.B.; Swank, R.T. *Hum. Mol. Genet.* 8, 323-330, 1999

A;Title: The beta3A subunit gene (*Ap3b1*) of the AP-3 adaptor complex is altered in the mouse hypopigmentation mutant pearl, a model for Hermansky-Pudlak syndrome and night blindness.

A:Reference number: z18864; MUID:99135912; PMID:9931340

A:Accession: T18295

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Seatus: predominantly

A:Residues: 1-1105 <FFND>

A_n-Residues: T-1165 (PEN) A-Gross-references: FMBL-AE103809; NID:q3885987; PID:q3885988; PTDN: AAC78338_1

A;Experimental source: strain C3H/HeJ

A; Experimente S: Sonatina

C; Genetics:

A; Gene: Ap3b1

Query Match 7.4%; Score 94; DB 2; Length 1105;
Best Local Similarity 21.2%; Pred. No. 6.5;
Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

Qy 1. MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRSVAAQNSAEVVRCLNSALQVGCGAFACL 60
 :||: :|: :: | :||: | | | :|| | . :| :
 Pb 308. LIOSPNAAWVMAVAQIYWH-----TSPKSE--AGVLSKSIVRLLBSNREVOYITVLONI 35

QY 61 ENSTCDTDGMYD-ICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFL----- 109

Qy 110 -----AIRRCSTFQRMIAEVQEECYSKLNVCASIARKNPEAITE---VVQLPNHFS 156

Qy 157 NRYYNRLVRSLL-E-CDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRR 215

Qy 216 TNEPQLKVLLRNLGEED 234

23

RESULT 9

T50776

hypothetical protein [imported] - *Vitis vinifera*

C; Species: *Vitis vinifera*

R;Matsumoto, S.; Dry, I.B.; Thomas, M.
DNA Seq. 8, 109-112, 1997
A;Title: Nucleotide sequence of grapevine (*Vitis vinifera*) cDNA similar to SNAP proteins.
A;Reference number: Z25233
A;Accession: T50776
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-289 <MAT>
A;Cross-references: EMBL:AB001375; PIDN:BAA19246.1
A;Experimental source: strain Shiraz

Query Match 7.1%; Score 90.5; DB 2; Length 289;
Best Local Similarity 19.9%; Pred. No. 2.7;
Matches 41; Conservative 33; Mismatches 95; Indels 37; Gaps 5;

Qy 8 LLVLVISASATHEAEQNDSVSPRKSRRVAQNSAEVVRCILNSALQVGCGAFACLENSTCDT 67
| :: | : | || | : : : | : || | | : | : | : | : | : |
Db 59 LSTVIQSSDSKHEAAQ-AYADAGHCYKKTSAKEAISCLEQA-----AYLFLDNGRFNM 110

Qy 68 DG-----MYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQR 119
| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 111 AGKYYKEIAELYELEQNFEQAIIFYFEKAADIYQSEEATTAAANQCNAKVAQFAAQLEQYQK 170

Qy 120 MIAEVQECCYSKLN-----VCSIAKRNPEAITEVQL----PNHFSNR 158
| : : | | : | : | : | : | : | : | : | : | : | : |
Db 171 AIQIYEDIGRPSLNNNLLKYGVKGHLLNAGICQLCKGDVVAITNALDRYQEMDPTFSGTR 230

Qy 159 YYNRLVRSLLCDEDTVSTIRDSLME 184
| | | | : | : | : | : |
Db 231 EYKLLVDLAAAVDEEDVVKFTDAVKE 256

RESULT 10
T38690
probable regulatory protein - fission yeast (*Schizosaccharomyces pombe*)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C;Accession: T38690
R;Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21805
A;Accession: T38690
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-783 < BRO>
A;Cross-references: EMBL:Z99568; PIDN:CAB16735.1; GSPDB:GN00066; SPDB:SPAC3C7.04
A;Experimental source: strain 972h-; cosmid c3C7
C;Genetics:
A;Gene: SPDB:SPAC3C7.04
A;Map position: 1
C;Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear cluster homology
F;35-71/Domain: GAL4 zinc binuclear cluster homology <GL4>

Query Match 7.1%; Score 90.5; DB 2; Length 783;
Best Local Similarity 23.3%; Pred. No. 8.7;

Matches 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;
 Qy 10 VLVISASATHEAEQNDSVSPRKSrv-----AAQNSAEVVRCLNSALQVGCGAF----- 57
 :::| :| || |: ||:: :| | : |: | :|
 Db 535 IIIMSRPVLHMKNAKNSPRVDRINEDCILAARHLISLVHLLQNHSQLSCYSFFDYNYT 594
 Qy 58 -----ACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCI----- 99
 |: |: | || : || : :| | : | :|
 Db 595 FSSALVVLLHCV-TEPCEED---DIAMQYAYSALDYMAEGNEAAKNCARVIRLFDAHLKG 650
 Qy 100 ----ANGVTSKV-FLAIRRCSTFQRMIAEVQ----EECYSKLNVCASIARKRNPEAITEVV 149
 || ||: |:| :|| |||| |: | | || :|
 Db 651 ARSDGNGNTSQSGFMA-----WQRWIAEVSAKDEPEKLMSPYNKSIGGGRNSNSLTPNA 704
 Qy 150 QLPNHFSNRYYNR-----LVRSILLECDEDTVSTIRDLSMEKIGPNMA--SLFHILQTD 200
 | | | :: | | | :| : | : | |::| || :|
 Db 705 NLGADVS--FFPTDDTSFLLDHSKLDDLEKFASTLDPI--KTPDLANDSSLLNWANTD 760

RESULT 11

T01491

ubiquitin-protein ligase homolog F17O7.15 - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
 C;Accession: T01491
 R;Vysotskaiia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, J.; Araujo, R.; Au, M.; Brendel, V.; Buehler, E.; Conway, A.B.; Conway, A.R.; Dewar, K.; Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.A.; Theologis, A.
 submitted to the EMBL Data Library, June 1998
 A;Description: *Arabidopsis thaliana* chromosome 1 BAC F17O7 sequence.
 A;Reference number: Z14334
 A;Accession: T01491
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1126 <VYS>
 A;Cross-references: EMBL:AC003671; NID:g2833627; PID:g3176690; GSPDB:GN00059;
 ATSP:F17O7.15
 A;Experimental source: cultivar Columbia
 C;Genetics:
 A;Gene: ATSP:F17O7.15
 A;Map position: 1
 A;Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2
 C;Superfamily: ubiquitin-protein ligase homology
 F;756-1120/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 7.1%; Score 89.5; DB 2; Length 1126;
 Best Local Similarity 22.1%; Pred. No. 16;
 Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;
 Qy 14 SASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACLENSTCD----- 66
 |: |:|| ||: || | ||: | ||: | |::| :|:
 Db 412 SSETQKDAESELVARRK-----NCAEL---YNIFLQLP-----QSDLNCNLCLMLGY 455
 Qy 67 ---TDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAE 123
 :| :| : | | | : | : | :|:|::| : | : | | | :|

```

Db      456 EGLSDKIYSLAGEVLKKLAAVDVTHRKFTKELSELASGLSSSTVRVLATLSTTQKM--- 512
Qy      124 VQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLECDEDTVSTIR---- 179
Db      513 -----SQNTCSMA---GASILRVLQVLSSLTTIDDSNVGTDKETDQEEQNIMQGLKV 562
Qy      180 --DSLMEKIGPNMASLFHILQTDHCAQT 205
Db      563 ALEPLWQELGQCIS--MTELQLDHTAAT 588

```

RESULT 12

T08121

peroxidase (EC 1.11.1.7) - flax (fragment)

C;Species: Linum usitatissimum (flax)

C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 04-Mar-2000

C;Accession: T08121

R;Omann, F.; Tyson, H.

submitted to the EMBL Data Library, February 1998

A;Description: cDNA sequence of a basic peroxidase (FLXPER4) in flax.

A;Reference number: Z16366

A;Accession: T08121

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-305 <OMA>

A;Cross-references: EMBL:AF049881; NID:g2944416; PIDN: AAC05277.1; PID:g2944417

A;Experimental source: cv. Stormont Cirrus

C;Genetics:

A;Gene: PER4

C;Superfamily: peroxidase

C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase

F;23-103/Disulfide bonds: #status predicted

F;50/Active site: Arg #status predicted

F;54,181/Binding site: heme iron (His) (axial ligands) #status predicted

F;56-61/Disulfide bonds: #status predicted

F;109-301/Disulfide bonds: #status predicted

F;188-213/Disulfide bonds: #status predicted

```

Query Match          7.0%;  Score 89;  DB 2;  Length 305;
Best Local Similarity 21.9%;  Pred. No. 3.8;
Matches   57;  Conservative  39;  Mismatches  92;  Indels   72;  Gaps    15;

```

```

Qy      11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGA-FACLE-NSTCDTD 68
Db      65 LLLDDTATFTGEKN--AGPNQNSV---RGFDIIDTIKTRVEAACNATVSCADILALAARD 119
Qy      69 GMYDI-----CKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLA----- 110
Db      120 GVVLVGGPTWTVPLGRRDARTASQSAANAQIPAPG---SSLGTITNLFTNKGLTARDVTI 176
Qy      111 -----IRRCTFQRMIAEVQEECYSKLNV---CSIAKRN-PEA-----ITEVVQLP 152
Db      177 LSGAHTIGQARCTTFRQRI-----YNDTNIDPAFATTRRGNCPQAGAGANLAPLDGTP 229
Qy      153 NHFSNRYYNRLV--RSLLECDEDTVST-IRDSLMEKIGPNMASLFHILQTDHCAQ---- 204
Db      230 TQFDNRYYQDLVARRGLHSDQELFNNGTQDALVRTYSNNAAT---FATDFAAAMVRMG 285

```

Qy 205 -----THPRADFNRRRTN 217
| : || || |
Db 286 NISPLTGTNGEIRFNCRRPN 305

RESULT 13

T45954

hypothetical protein F7J8.120 - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C:\Date: 04-Feb-2000 #sequence revision 04-Feb-2000 #text change 20-Jun-2000

C:Accession: T45954

R; Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.

submitted to the Protein Sequence Database, January 2000
Accession number: Z23018

A; Reference number: Z23018

A;Accession: T45954

A; Status: preliminary

A;Molecule type: DNA

A;Residues: 1-473 <BEV>

A;Cross-references: EMBL:AL137189

A; Experiments

C; Genetics:

A;Map position: 5

A; Introns: 29/1;

A;Note: F7J8.120

C:Superfamily: Arabidopsis thaliana hypothetical protein F7J8.130

Query Match 6.9%; Score 88; DB 2; Length 473;
Best Local Similarity 22.6%; Pred. No. 7.9;
Matches 54; Conservative 42; Mismatches 103; Indels 40; Gaps 13;

Qy 27 VSPRKS R VAAQ N SAEV VR CLN S AL QVGCGA F A CLEN -- STCD -- TDG MYDICKS - FLY 79
: | : | : | : | : | : | : | : | : | : | : | : | : |

Qy 80 SAAKFDTQGKAF----VKESLKCIANGVTSKVFLAIRRCSTFQRMIAE---VQEEC-- 128

Db 76 PKNIREAQYRNFKLNIDTNESSLKCFG----CRFFSICRMCNSFNTSLCKCGKLMNEEISF 131

Db 132 LEYEENDVEGVFMRDKSSFIITDDLRLTDDST---SSLQLTLKDLGCADVSKLREQVLD 187

RESULT 14

RE56B1
S45628

DNA-directed DNA polymerase (EC 2.7.7.7) alpha 180K chain - mouse

N:Alternate names: DNA polymerase alpha/DNA primase complex 180K chain

C:Species: *Mus musculus* (house mouse)

C.Species: Mus musculus (house mouse)
C.Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 27-Oct-2003

C:Accession: S45638: M16642

R;Stadlbauer, F.; Brueckner, A.; Rehfuss, C.; Eckerskorn, C.; Lottspeich, F.; Foerster, V.; Tseng, B.Y.; Nasheuer, H.P.
Eur. J. Biochem. 222, 781-793, 1994
A;Title: DNA replication in vitro by recombinant DNA-polymerase-alpha-primase.
A;Reference number: S45628; MUID:94298818; PMID:8026492
A;Accession: S45628
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1465 <STA>
A;Cross-references: EMBL:D17384; NID:g397829; PIDN:BAA04202.1; PID:g442471
R;Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Ui, M.; Hanaoka, F.
J. Biol. Chem. 268, 8111-8122, 1993
A;Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA polymerase alpha-primase complex and their gene expression during cell proliferation and the cell cycle.
A;Reference number: A46642; MUID:93216788; PMID:8463324
A;Accession: A46642
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 4-1465 <MIY>
A;Experimental source: FM3A cells
A;Note: sequence extracted from NCBI backbone (NCBIN:129146, NCBIP:129147)
C;Superfamily: DNA polymerase
C;Keywords: DNA binding; nucleotidyltransferase; nucleus

Query Match 6.9%; Score 87.5; DB 2; Length 1465;
Best Local Similarity 20.7%; Pred. No. 33;
Matches 34; Conservative 32; Mismatches 55; Indels 43; Gaps 7;

Qy 6 AVLLVLVISASAT-----HEAEQNDSVSPRKSRAAQNSAEVVRLNSALQVGCGAFA 58
 |||: | : | : |::|:|:||::|:|:|:|:|:|:|:|:|:|
Db 1236 AVLIALWLGLDSTQFRVHQYHKDEENDALLGGPAQLTDEEKYK-----DCEKFK 1284

Qy 59 CLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT-----SKVFLAIR 112
 ||| | | |:|:|| ::|:|:|:|:|:|:|:|:|:|
Db 1285 CLCPS-CGTENIYD---NVFEGSGLDMEPSLYRCSNVDCKVSPLTFMVQLSNKLIMDIR 1339

Qy 113 RCSTFQRMIAEVQEECYSKLNVCASIARKRNPEAITEVVQLPNHFS 156
 ||| ::| :| | :|:|:|:|:|:
Db 1340 RCI-----KKYYDGWLIC---EEPTCCSRLRRPLHFS 1369

RESULT 15

H72097

mg++ transporter (cbs domain) - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: H72097
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Davis, R.W.; Stephens, R.S.
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: H72097
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-470 <ARN>
A;Cross-references: GB:AE001613; GB:AE001363; NID:g4376550; PIDN:AAD18435.1;
PID:g4376560
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: mgtE
C;Superfamily: magnesium transport protein mgtE

Query Match 6.8%; Score 86; DB 2; Length 470;
Best Local Similarity 22.9%; Pred. No. 12;
Matches 47; Conservative 33; Mismatches 61; Indels 64; Gaps 13;

Qy 56 AFACLENSTCDTD-GMYDICK-----SFLYSAAKFDTQGKAFVKE~~S~~LKCIANGVT~~S~~K 106
|| || || :|: | : : :| : :| || |:|
Db 19 AFTCL----STDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCI---TAK 69

Qy 107 VFLAIR----RCSTFQRMIAEVQE~~E~~CYSKLN~~V~~CSIAKRNP--EAITEVVQLPNHFSNR~~Y~~ 159
| | | | :|: | | | :| :| | | :| :| :|
Db 70 VAFIINTDSASRWAI~~F~~RRL----SDSEVCALIEQMPPDEAVWVLDDIP---DRR 116

Qy 160 YNRLVRSLL~~E~~CDED~~T~~V~~S~~TIRDSLMEKIGPNMA-----SLFHIL-----QTDHCAQTHP 207
| |:: : | | | | :| | | | | | | | :|
Db 117 YRRILELI--DSKKALKIRD--LQKHGRNTAGRLMTNEFFAFLMETTVKDVSACIRSNP 171

Qy 208 RADFNRRRTNEPQKLKVLLRNLRGE 232
| | | | :| :| :|
Db 172 GIDLTR-----LVFVLDFKGE 187

Search completed: July 19, 2004, 15:33:57
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: July 19, 2004, 15:33:34 ; Search time 46 Seconds
(without alignments)
1678.315 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1285345 seqs, 312560633 residues

Total number of hits satisfying chosen parameters: 1285345

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
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1	1268	100.0	247	9	US-09-840-989A-2	Sequence 2, Appli
2	1268	100.0	247	9	US-09-361-736-10	Sequence 10, Appli
3	1268	100.0	247	13	US-10-116-051-2	Sequence 2, Appli
4	1268	100.0	247	14	US-10-177-293-441	Sequence 441, App
5	1268	100.0	247	14	US-10-418-226-10	Sequence 10, Appli
6	1268	100.0	247	15	US-10-465-572-18	Sequence 18, Appli
7	1268	100.0	247	15	US-10-372-683-41	Sequence 41, Appli
8	937	73.9	276	9	US-09-925-300-1426.	Sequence 1426, Ap
9	662.5	52.2	256	9	US-09-840-989A-3	Sequence 3, Appli
10	660.5	52.1	204	13	US-10-116-051-10	Sequence 10, Appli
11	628	49.5	170	9	US-09-361-736-9	Sequence 9, Appli
12	628	49.5	170	14	US-10-418-226-9	Sequence 9, Appli
13	358	28.2	70	9	US-09-864-761-37770	Sequence 37770, A
14	354	27.9	302	12	US-10-058-270A-22	Sequence 22, Appli
15	354	27.9	302	12	US-10-364-889-4	Sequence 4, Appli
16	354	27.9	302	14	US-10-177-293-443	Sequence 443, App
17	354	27.9	302	14	US-10-338-395-23	Sequence 23, Appli
18	354	27.9	302	14	US-10-418-226-12	Sequence 12, Appli
19	354	27.9	302	15	US-10-295-027-100	Sequence 100, App
20	354	27.9	302	15	US-10-173-999-80	Sequence 80, Appli
21	351.5	27.7	251	14	US-10-418-226-2	Sequence 2, Appli
22	333.5	26.3	251	9	US-09-361-736-2	Sequence 2, Appli
23	303	23.9	118	13	US-10-116-051-9	Sequence 9, Appli
24	95.5	7.5	299	12	US-10-282-122A-49895	Sequence 49895, A
25	91	7.2	901	10	US-09-828-062-8	Sequence 8, Appli
26	91	7.2	901	16	US-10-768-511-8	Sequence 8, Appli
27	90.5	7.1	783	16	US-10-149-310-96	Sequence 96, Appli
28	90	7.1	281	12	US-09-973-278-172	Sequence 172, App
29	90	7.1	281	12	US-09-973-278-277	Sequence 277, App
30	90	7.1	331	15	US-10-264-049-2324	Sequence 2324, Ap
31	89.5	7.1	622	16	US-10-437-963-161551	Sequence 161551,
32	89.5	7.1	1123	12	US-10-282-122A-70581	Sequence 70581, A
33	89.5	7.1	10203	16	US-10-661-809-23	Sequence 23, Appli
34	86	6.8	401	12	US-10-425-114-63193	Sequence 63193, A
35	86	6.8	470	12	US-10-282-122A-54827	Sequence 54827, A
36	86	6.8	500	15	US-10-289-762-299	Sequence 299, App
37	85.5	6.7	564	12	US-10-424-599-272057	Sequence 272057,
38	85	6.7	281	12	US-10-424-599-172444	Sequence 172444,
39	84.5	6.7	402	16	US-10-437-963-184603	Sequence 184603,
40	83.5	6.6	331	12	US-10-464-261-3	Sequence 3, Appli
41	83.5	6.6	331	12	US-10-464-261-4	Sequence 4, Appli
42	83.5	6.6	1027	12	US-10-654-416-8	Sequence 8, Appli
43	83.5	6.6	1029	12	US-10-654-416-6	Sequence 6, Appli
44	83	6.5	398	12	US-10-282-122A-71213	Sequence 71213, A
45	82.5	6.5	450	12	US-10-425-114-58956	Sequence 58956, A

ALIGNMENTS

RESULT 1

US-09-840-989A-2

; Sequence 2, Application US/09840989A

; Patent No. US20020042372A1

; GENERAL INFORMATION:

; APPLICANT: Olsen et al.

; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods
Based Thereon
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-989A-2

Query Match 100.0%; Score 1268; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.5e-125;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACL 60
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Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDVTSTIRD 180
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Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDVTSTIRD 180

Qy 181 SIMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Db 181 SIMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
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Db 241 RTSHESA 247

RESULT 2

US-09-361-736-10

; Sequence 10, Application US/09361736
; Patent No. US20020102634A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA

; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,529
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN

US-09-361-736-10

Query Match 100.0%; Score 1268; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.5e-125;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACL 60
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Qy 61 ENSTCDTDGYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180
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Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
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Db 241 RTSHESA 247

RESULT 3
US-10-116-051-2
; Sequence 2, Application US/10116051

; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIocalcIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-051-2

Query Match 100.0%; Score 1268; DB 13; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.5e-125;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Qy	121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180
Db	121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180
Qy	181 SIMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db	181 SIMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Qy	241 RTSHESA 247
Db	241 RTSHESA 247

RESULT 4

US-10-177-293-441
; Sequence 441, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen

; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puszta, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION,
ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 441
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-177-293-441

Query Match 100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.5e-125;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL	60
Db	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL	60
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRM	120
Db	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRM	120
Qy	121	IAEVQEECYSKLNVCSTIAKRNPPEAITEVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD	180
Db	121	IAEVQEECYSKLNVCSTIAKRNPPEAITEVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD	180
Qy	181	SIMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Db	181	SIMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240

Qy 241 RTSHESA 247
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Db 241 RTSHESA 247

RESULT 5

US-10-418-226-10

; Sequence 10, Application US/10418226
; Publication No. US20030181663A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D2
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human

US-10-418-226-10

Query Match 100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.5e-125;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL 60
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Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
: |||||||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180
: |||||||
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
: |||||||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
: |||||
Db 241 RTSHESA 247

RESULT 6

US-10-465-572-18

; Sequence 18, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Riggins, Gregory
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.00012
; CURRENT APPLICATION NUMBER: US/10/465,572
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201,642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307,600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-465-572-18

Query Match 100.0%; Score 1268; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.5e-125;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 7

US-10-372-683-41

; Sequence 41, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683

; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 41
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-41

Query Match 100.0%; Score 1268; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.5e-125;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNAAEVVRCLNSALQVGCGAFACL 60
|||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNAAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
|||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
|||
Db 121 IAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240
|||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240

Qy 241 RTSHESA 247
|||
Db 241 RTSHESA 247

RESULT 8

US-09-925-300-1426

; Sequence 1426, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1426
; LENGTH: 276
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (273)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (275)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1426

Query Match 73.9%; Score 937; DB 9; Length 276;
Best Local Similarity 99.5%; Pred. No. 4.8e-90;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL	60
Db	89	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL	148
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Db	149	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	208
Qy	121	IAEVQEECYSKLNVCASIARKRNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD	180
Db	209	IAEVQEECYSKLNVCASIARKRNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD	268
Qy	181	SLMEKI 186	
Db	269	SLMEXI 274	

RESULT 9

US-09-840-989A-3

; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods
Based Thereon
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-09-840-989A-3

Query Match 52.2%; Score 662.5; DB 9; Length 256;
 Best Local Similarity 53.4%; Pred. No. 3.6e-61;
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

Qy	11 LVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTG 70
	: : : : : :: : ::
Db	12 LVLGTAATFDTPDEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTG 70
Qy	71 YDICKSFLYSAAKFDTQGKAFVKESSLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
	: : :: : : : :
Db	71 HDICQLFFHTAATFNTQGKTFVKESSLRCIANGVTSKVFTIRRCGVFQRMISEVQEECYS 130
Qy	131 KLNVCASIARKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRDLSLMEKIGPNM 190
	: : : : : : : : : : : : :
Db	131 RLDICGVARSNPEAIGEVVQVPAHFNPYYSTLLQSLACDEETVAVVRAGLVARLGPD 190
Qy	191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
	: : : : : : : : :
Db	191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241

RESULT 10

US-10-116-051-10

; Sequence 10, Application US/10116051
 ; Publication No. US20020146791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olsen et al.
 ; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIocalcin
 ; FILE REFERENCE: PF108P1D1C1
 ; CURRENT APPLICATION NUMBER: US/10/116,051
 ; CURRENT FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: 09/312,610
 ; PRIOR FILING DATE: 1999-05-17
 ; PRIOR APPLICATION NUMBER: 08/431,117
 ; PRIOR FILING DATE: 1995-04-28
 ; PRIOR APPLICATION NUMBER: 08/208,005
 ; PRIOR FILING DATE: 1994-03-08
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 204
 ; TYPE: PRT
 ; ORGANISM: Oncorhynchus kisutch

US-10-116-051-10

Query Match 52.1%; Score 660.5; DB 13; Length 204;
 Best Local Similarity 60.8%; Pred. No. 4.3e-61;
 Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

Qy	11 LVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTG 70
	: : : : : :: : ::
Db	12 LVLGTAATFDTPDEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTG 70
Qy	71 YDICKSFLYSAAKFDTQGKAFVKESSLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
	: : :: : : : :
Db	71 HDICQLFFHTAATFNTQGKTFVKESSLRCIANGVTSKVFTIRRCGVFQRMISEVQEECYS 130

Qy 131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRDSLMEKIGPNM 190
Db :|::| :|: ||||| ||||:| || |||: |::||| |||:||: :| |: ::|||:
131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVRAGLVARLGPDM 190

Qy 191 ASLFHILQTDHCAQ 204
Db :|| :|| || |
191 ETLFQLLQNKHCPQ 204

RESULT 11

US-09-361-736-9

; Sequence 9, Application US/09361736
; Patent No. US20020102634A1

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Human Stanniocalcin-alpha

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/361,736

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/460,529

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: MULLINS, J.G.

; REGISTRATION NUMBER: 33,073

; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 AMINO ACIDS

; TYPE: AMINO ACID

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

US-09-361-736-9

Query Match 49.5%; Score 628; DB 9; Length 170;

Best Local Similarity 66.5%; Pred. No. 8.8e-58;

Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Qy	28	SPRKSRAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGYDICKSFLYSAAKFDTQ	87
	: : : :: : : : : :		
Db	1	SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNDGMHEICRSFLHGAAKFDTQ	60
Qy	88	GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCASIARKNPEAITE	147
	: : : : : : :		
Db	61	GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVQAQNPEAMGE	120
Qy	148	VVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRDLSMEKIGPNMASLFHIL	197
	: : : :: : : : :		
Db	121	VAQVPSQFPNRYYSTLLQSLLTCDDETVEQVRAGLVSRLPEMGVLFQLL	170

RESULT 12

US-10-418-226-9

; Sequence 9, Application US/10418226

; Publication No. US20030181663A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc

; TITLE OF INVENTION: Human Stanniocalcin-Alpha

; FILE REFERENCE: PF143P1D2

; CURRENT APPLICATION NUMBER: US/10/418,226

; CURRENT FILING DATE: 2003-04-18

PRIOR APPLICATION NUMBER: 09/3

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: 08/

; PRIOR FILING DATE: 1995-06-02

; PRIOR APPLICATION NUMBER: PCT

; PRIOR FILING DATE: 1994-11-30

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.

; SEQ ID NO 9

; LENGTH: 1

; TYPE: PRT

; ORGANISM:

US-10-418-226-9

Query Match 49.5%; Score 628; DB 14; Length 170;
Best Local Similarity 66.5%; Pred. No. 8.8e-58;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Qy 28 SPRKS R VAAQNSAEV VRCL NSALQVGCGAFACLENSTCD TDG MYDICKSFLYSAAKFDTQ 87
| | : | : | : :: | || || | || || | : || || : || || : || | : || || |
Pb 1 SPRTA PESASSPSDVARGLNCALQVCGSAEAGLDNSTCNTDMH ELCRSEI LGA AAKFDTQ 60

Qy 88 GKAFVKESLKCIANGVTSKVLAIRRCSTFQRMIAEVQEECYSKLNVCASIAKRNPEAITE 147
|| | | | | | | | | : | | | | | | | | : | | | | : | | | | | | | | : | | | | : | | | | : |

Qy 148 VVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRDSLMEKIGPNNMASLFHIL 197
| :|: | ||||: |::||| |||||| :| |: :: | | || :|

RESULT 13

US-09-864-761-37770

; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37770
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012119.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7

; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUE 3.00e-35
; OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUE 3.00e-34

US-09-864-761-37770

Query Match 28.2%; Score 358; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.9e-30;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	88	GKAFVKESLKCIANGVTSKVFLAIRCSTFQRMIAEVQEECYSKLNVCASI	KRNPEAITE	147
Db	1	GKAFVKESLKCIANGVTSKVFLAIRCSTFQRMIAEVQEECYSKLNVCASI	KRNPEAITE	60
Qy	148	VVQLPNHFSN	157	
Db	61	VVQLPNHFSN	70	

RESULT 14

US-10-058-270A-22

; Sequence 22, Application US/10058270A
; Publication No. US20040029114A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-005210US
; CURRENT APPLICATION NUMBER: US/10/058,270A
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 302
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-058-270A-22

Query Match 27.9%; Score 354; DB 12; Length 302;
Best Local Similarity 32.4%; Pred. No. 1.5e-28;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL 60
| ||::: ||: | | | : | |:: ||:||: || : | |||| |
Db 12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRM 120
||::|: |:: || :||::| ||| |||:||:||:|| |: : | :| : |
Db 72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIDALKCKAHALRHRCGCISRKCPAIREM 131

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180
::::| ||| | ::|: |: | | |:: : : | || | | | |: |
Db 132 VSQLQRECYLKHDLCAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLTCGEEVKEAITH 191

Qy 181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL----- 222
|: : | || | | | | | | |: : | |
Db 192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251

Qy 223 KVLLRNLRGEEDSPSH 238
: | :| | | |
Db 252 RETGRGAKGERGSKSH 267

RESULT 15

US-10-364-889-4

; Sequence 4, Application US/10364889
; Publication No. US20030224989A1
; GENERAL INFORMATION:
; APPLICANT: Pahel, Gregory L.
; APPLICANT: Quinn, Kerry
; TITLE OF INVENTION: Compositions and Methods for Treatment of Osteoarthritis
; FILE REFERENCE: 21402-558
; CURRENT APPLICATION NUMBER: US/10/364,889
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/356,376
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-889-4

Query Match 27.9%; Score 354; DB 12; Length 302;
Best Local Similarity 32.4%; Pred. No. 1.5e-28;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL 60
| ||::: ||: | | | : | |:: ||:||: || : | |||| |
Db 12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCAHALRHRFGCISRKCPAIREM 131

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
:::|:|:|:|:|:|:|:|:|:
Db 132 VSQQLQRECYLKHDLCQAQENTRVIVEMIHFKDLLLHEPYVDLVNLLTCGEEVKEAITH 191

Qy 181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL----- 222
|:|:|:|:|:
Db 192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251

Qy 223 KVLLRNLRGEEDSPSH 238
:|:|:|:
Db 252 RETGRGAKGERGSKSH 267

Search completed: July 19, 2004, 15:39:03
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2004, 15:29:43 ; Search time 39 Seconds
(without alignments)
1998.282 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rat:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description

1	1199	94.6	247	6	Q9N0T1	Q9n0t1 bos taurus
2	1192.5	94.0	246	11	Q7TSN9	Q7tsn9 mus musculu
3	779.5	61.5	252	13	Q800I4	Q800i4 lepisosteus
4	778.5	61.4	252	13	Q800I5	Q800i5 amia calva
5	654	51.6	249	13	Q98TB7	Q98tb7 osteoglossu
6	354.5	28.0	296	11	Q9DCS6	Q9dcs6 mus musculu
7	102	8.0	473	10	Q9SZ16	Q9sz16 arabidopsis
8	92	7.3	1108	11	Q91YR4	Q91yr4 mus musculu
9	91.5	7.2	1068	5	Q8IHR6	Q8ihr6 plasmodium
10	90.5	7.1	454	5	Q9GV74	Q9gv74 dictyosteli
11	90.5	7.1	783	3	O14130	O14130 schizosacch
12	89.5	7.1	622	10	Q8H2Y0	Q8h2y0 oryza sativ
13	89.5	7.1	1126	10	O64605	O64605 arabidopsis
14	89.5	7.1	3658	10	Q9M7K6	Q9m7k6 arabidopsis
15	89.5	7.1	9439	16	Q8CP76	Q8cp76 staphylococ
16	89	7.0	305	10	O65029	O65029 linum usita
17	89	7.0	996	13	Q7ZW18	Q7zw18 brachydanio
18	89	7.0	1728	10	Q9LUI2	Q9lui2 arabidopsis
19	88	6.9	473	10	Q9LFC2	Q9lfc2 arabidopsis
20	87	6.9	578	10	Q8LEG3	Q8leg3 arabidopsis
21	86.5	6.8	290	10	Q8LSZ6	Q8lsz6 hevea brasi
22	86	6.8	470	16	Q9Z8Q2	Q9z8q2 chlamydia p
23	86	6.8	510	10	Q9LFC4	Q9lfc4 arabidopsis
24	86	6.8	556	3	Q03899	Q03899 saccharomyc
25	86	6.8	1091	6	Q7YRF1	Q7yrf1 canis famil
26	85.5	6.7	183	10	Q8L5G9	Q815g9 hevea brasi
27	85.5	6.7	290	10	Q8L5B7	Q815b7 hevea brasi
28	85.5	6.7	290	10	Q948Q0	Q948q0 hevea brasi
29	85.5	6.7	447	3	Q7Z9L8	Q7z918 coprinus ci
30	85.5	6.7	634	5	Q95PL8	Q95pl8 trypanosoma
31	85.5	6.7	654	16	Q8CN27	Q8cn27 staphylococ
32	85	6.7	806	10	Q9FFZ5	Q9ffz5 arabidopsis
33	83.5	6.6	290	10	Q8L3V1	Q813v1 hevea brasi
34	83.5	6.6	290	10	Q8L5H1	Q815h1 hevea brasi
35	83.5	6.6	427	5	Q9N3E2	Q9n3e2 caenorhabdi
36	83.5	6.6	1026	3	O74669	O74669 pneumocysti
37	83.5	6.6	1028	3	O74668	O74668 pneumocysti
38	83.5	6.6	1273	5	Q9BL02	Q9b102 caenorhabdi
39	83	6.5	250	17	Q04927	Q04927 methanobact
40	83	6.5	260	10	Q8GZS0	Q8gzs0 lupinus alb
41	83	6.5	297	12	Q91BJ2	Q91bj2 spodoptera
42	83	6.5	365	10	Q9SU53	Q9su53 arabidopsis
43	83	6.5	398	16	Q8CRY1	Q8cry1 staphylococ
44	83	6.5	848	6	Q9XS94	Q9xs94 bos taurus
45	83	6.5	1431	16	Q891P4	Q891p4 clostridium

ALIGNMENTS

RESULT 1

Q9N0T1

ID Q9N0T1 PRELIMINARY; PRT; 247 AA.

AC Q9N0T1;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Stanniocalcin.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA DiMattia G.E.;
 RT "bovine stanniocalcin cDNA sequence.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF257506; AAF68996.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 SQ SEQUENCE 247 AA; 27555 MW; F9942A715E2A3DE0 CRC64;

Query Match 94.6%; Score 1199; DB 6; Length 247;
 Best Local Similarity 94.7%; Pred. No. 1.5e-105;
 Matches 234; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY	1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQN SAEVVRC LNSALQVGCGA FACL 60
	: : : : : : : :
Db	1 MLQNSAVILVLVISASATHEAEQNDSVSLRKSRVA AQN SAEVIRCL NSALQVGCGA FACL 60
QY	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLK CIANGVT SKVFLAIRRC STFQRM 120
	: : : : : : : :
Db	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLK CIANGVT SKVFLAIRRC STFQRM 120
QY	121 IAEVQEECYSKLNVC SIAKRNP EAITEVVQLPNHFSNRYY NLVRSLLECD EDTVSTIRD 180
	: : : : : : :
Db	121 IAEVQEECYT KLNVC SVAKRNP EAITEVVQLPNHFSNRYY NLVRSLLD CEDDTVSTIRD 180
QY	181 SLMEKIGPNMASLFHILQTDHCAQTHPRADEFNRRRTNEPQKLKVLLRNLRGEEDSP SHIK 240
	: : : : : : :
Db	181 SLMEKIGPNMASLFHILQTDHCAHTQQRADFNRRRANE P QKLKVLLRNLRGEASP SHIK 240
QY	241 RTSHESA 247
Db	241 RTSQESA 247

RESULT 2

Q7TSN9

ID Q7TSN9 PRELIMINARY; PRT; 246 AA.
 AC Q7TSN9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Stanniocalcin 1.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RA Chang A.C., Cha J., Reddel R.R.;
 RT "The murine stanniocalcin 1 gene is not essential for growth and
 development.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF512563; AAP47156.1; -.
 SQ SEQUENCE 246 AA; 27423 MW; 4101C37EB6D743B2 CRC64;

 Query Match 94.0%; Score 1192.5; DB 11; Length 246;
 Best Local Similarity 93.9%; Pred. No. 6.3e-105;
 Matches 232; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

 Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSALQVGCGAACL 60
 |||||||::| |||||:| |||||||:| ||||||||||||||||||||||||||| :: | |||||
 Db 1 MLQNSAVILALVISAAAHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSACRLAAG-FACL 59

 Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 60 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 119

 Qy 121 IAEVQECCYSKLNVCASIARKNPEAITEEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 120 IAEVQECCYSKLNVCASIARKNPEAITEVIQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 179

 Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 180 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 239

 Qy 241 RTSHESA 247
 ||| |||
 Db 240 RTSQESA 246

RESULT 3

Q80014

ID Q800I4 PRELIMINARY; PRT; 252 AA.

AC Q800I4;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Stanniocalcin precursor.

GN STC.

OS Lepisosteus osseus (Long-nosed gar).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;

OC Lepisosteus.

OX NCBI TaxID=34771;

RN [1]

RP SEQ

RA Amemiya Y., Youson J.H.;

RT "Primary structure of sta

RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB106623; BAC66164.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1..
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 KW Signal.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 252 Potential.
 SQ SEQUENCE 252 AA; 27936 MW; 2C99E88DCCED2E33 CRC64;

 Query Match 61.5%; Score 779.5; DB 13; Length 252;
 Best Local Similarity 59.8%; Pred. No. 9.5e-66;
 Matches 152; Conservative 44; Mismatches 49; Indels 9; Gaps 3;

 Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRLNSALQVGCGAFACL 60
 ||: : : ||: ||: || : | : ||: | |||: : ||: : :: | ||||||| ||||| |||||
 Db 1 MLRKIGLLLLVLLTSA-YELDQNESFSPPRTRVSTHPSDVARCLNSALQVGCGAFACL 59

 Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
 ||||| |||: ||| ||| ||| ||| ||| ||| ||| |||: ||| |||, ||| ||| |||
 Db 60 ENSTCDTDGMHDICKSFLYSAAKFDTQGKVFVKESLKCIANGITSKVFLTIRRCSTFQRM 119

 Qy 121 IAEVQEECYSKLNVCIAKRNPEAITEVQVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180
 |:||||| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 120 ISEVQEECYSKLIDICGVAKLPDAISEVAQLPSHPNRYYSKLLQSLMECDDETVSLVRS 179

 Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRAD-----FNRRRTNEPQKLKVLLRNLRGEE 233
 ||: :|| | || || :||: | : : | | | | | : ||| |
 Db 180 SLVSRLGPEMAMLFQLLQSKPCPSSSLSSPAGAEGRGNWRWPIGPHVFK-MQPQLRREP 238

 Qy 234 DSPSHIKRTSHESA 247
 : |:: :|:
 Db 239 STLFSKKRSADDSS 252

RESULT 4

Q800I5

ID Q800I5 PRELIMINARY; PRT; 252 AA.

AC Q800I5;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last seq

DT 01-OCT-2003 (TrEMBLrel. 25, Last ann

DE Stanniocalcin precursor.

GN STC.

OS Amia calva (Bowfin).

OC Eukaryota; Metazoa; Chordata; Craniata

OC Actinopterygii; Neopterygii; Amiiformes

OX NCBI_TaxID=7924;

RN [1]
BB SEQUENCE FROM N. 3

RP SEQUENCE FROM N.A.
PA Amniotic V. Yaman. I.U.

RA Ameliya I., Iouson S.H.,

RT "Primary structure of stanniocalcin in two basal Actinopterygii.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB106622; BAC66163.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 KW Signal.
 FT SIGNAL 1 .32 Potential.
 FT CHAIN 33 252 Potential.
 SQ SEQUENCE 252 AA; 27868 MW; B9D9663610DF0B5D CRC64;

 Query Match 61.4%; Score 778.5; DB 13; Length 252;
 Best Local Similarity 69.8%; Pred. No. 1.2e-65;
 Matches 141; Conservative 37; Mismatches 23; Indels 1; Gaps 1;

 Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAAQNSAEVVRCI NSALQVGCGAACL 60
 || : :||:||: || :| :||:| ||||:||:| :||:| |||||||:||:||:| |||||||:||:||:|
 Db 1 MLHKTGILLLVLLTSA-YELDQNESFSPPRTRVAHSSSDVARCLNSALQVGCGAACL 59

 Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
 |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 60 ENSTCDTDGMHDICKSFLYSAAKFDTQGKVFVKESLKCIANGITSKVFLTIRRCSTFQRM 119

 Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180
 :|:|||||:||:||:|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 120 ISEVQEECYTKLDICEVARLNPEAISEVAQLPSHPNRYYSKLLQSLMECDEETVS VVRS 179

 Qy 181 SLMEKIGPNMASLFHILQTDHC 202
 :|: :|| |: || :||: |
 Db 180 NLVSRLGP EMMSMLFQQLQSKPC 201

RESULT 5

Q98TB7
ID Q98TB7 PRELIMINARY; PRT; 249 AA.
AC Q98TB7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Stanniocalcin precursor.
GN STC.
OS Osteoglossum bicirrhosum (silver arawana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Osteoglossidae; Osteoglossum.
OX NCBI_TaxID=109271;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stannius corpuscles;
RA Amemiya Y., Marra L.E., Reyhani N., Youson J.H.;
RT "Stanniocalcin from an ancient teleost. Evidence for a monomeric form

RT of the hormone and an extracorporeal distribution.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB060558; BAB43868.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004108; F:citrate (Si)-synthase activity; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
 DR InterPro; IPR002020; Citrate_synth.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 KW Signal.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 249 POTENTIAL.
 SQ SEQUENCE 249 AA; 27389 MW; 10297D054A2BEB3A CRC64;

Query Match 51.6%; Score 654; DB 13; Length 249;
 Best Local Similarity 57.5%; Pred. No. 7.5e-54;
 Matches 122; Conservative 43; Mismatches 45; Indels 2; Gaps 1;

QY	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCNSALQVGCGAFACL	60
	: : : :: : : : :: :		
Db	1	MIQKCMLLLFFLTASAFA--VIDQEEPSTRTRFAANSLSDVARCLSGALQVGCSAFACL	58

QY	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
	:: : : : : : :		
Db	59	ENSTCDTDGMHEICKTFLYTAAKFDTQGKTFVKESLRCMANGITSKGFLMVRRCSTFQSM	118

QY	121	IAEVQEECYSKLNVCASIARKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD	180
	: : : : : : : : : : : :		
Db	119	LADVQEDCYNKLDLCGVARANPEAIGEVAQLPNSFPNRHYSTLLQSLLECDQETVSLVRD	178

QY	181	SILMEKIGPNMASLFHILQTDHCAQTHPRADFN	212
	: : : : : : : :		
Db	179	SMSARLGPEVAMLFKLLQSSSRSGSAAQASNN	210

RESULT 6
 Q9DCS6
 ID Q9DCS6 PRELIMINARY; PRT; 296 AA.
 AC Q9DCS6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Stanniocalcin 2.
 GN STC2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK002527; BAB22164.1; -.
DR MGD; MGI:1316731; Stc2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
SQ SEQUENCE 296 AA; 32488 MW; BD8961CEFFA47508 CRC64;

Query Match 28.0%; Score 354.5; DB 11; Length 296;
Best Local Similarity 31.7%; Pred. No. 2.3e-25;
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

Qy 7 VLLVLVISASATHEAEQNDSVSP-----RKSRAAAQNSAEVVRCLN SALQVGCGA 56
| | || : | : || : | : | | : || : || : || : | : || | | |
Db 10 VTLALVF--ATLDPAQGTDSTNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVCGV 67

Qy 57 FACLENSTCDTDGYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCST 116
| | || :: | : | :: || : | : | | | | : | : | : | : | : | : |
Db 68 FECFENNNSCEIQGLHGICMTFLHNAGKFDAQGKSF IKDALRCKAHALRHKGFCISRKCPA 127

Qy 117 FQRMIAEVQEECYSKLNVCSI AKRNPEAITEV VQLPNHFSNRYY NRLVRSLL ECDED TVS 176
: | : :: | | | | : | : | | | | : | | | | | | | | | | | | | |
Db 128 IREMVFQLQRECYLKHDLC SAAQENGVIVEMIHFKD LLLLHEPYVDLVNLLT CGEDVKE 187

Qy 177 TIRDSLMEKIGPNMASLFHIL-----QTDHCAQTH---PRA DFNR RRTNEP QKLKV 224
: | : : | | | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 188 AVTRSVQAQCEQS WGG LCSILSFC TSNIQR PPTAAPEHQPLADRAQLSRPHHRD TDHHLT 247

Qy 225 LLRNL RGEEDSP SHIK----RTSHESA 247
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 248 ANRGAKGERGSKSHPN AHARGRTGGQSA 275

RESULT 7

Q9SZ16

ID Q9SZ16 PRELIMINARY; PRT; 473 AA.

AC Q9SZ16;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN F10M23.100 OR AT4G26760.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Lecharny A., Chefdor F., Krivitzky M., Kreis M.,
 RA Hoheisel J., Mewes H.W., Mayer K.F.X., Schueler C.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lecharny A., Chefdor F., Krivitzky M., Kreis M., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL035440; CAB36522.1; -.
 DR EMBL; AL161565; CAB79531.1; -.
 DR PIR; T04799; T04799.
 DR InterPro; IPR007145; MAP65_ASE1.
 DR Pfam; PF03999; MAP65_ASE1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 53737 MW; 8CB8B883CF5CCCD1 CRC64;

Query Match 8.0%; Score 102; DB 10; Length 473;
 Best Local Similarity 21.0%; Pred. No. 0.36;
 Matches 50; Conservative 43; Mismatches 67; Indels 78; Gaps 11;

Qy	26 SVSPRKSRVAAQNSAEVVRLNSALQVGCGAFACLENSTCDT----DGMYDICKSF-LYS 80
	: : : :: ::: : : :
Db	50 NVYKKKVELAAKSRAELLQTLSD-----ATVELSNLTALGEKSYIDICDSMSLFP 100

Qy	81 AAKFDTQGKAFVKESLKIA-----NG-- 102
	:
Db	101 LQPDKTSGT--IKEQLSAIAPALEQLWQQKEERVRAFSDVQSQIQKICEEIAGGLNNGPH 158

Qy	103 VTSKVFLAIRRCSTFQRMIAEVQEECYSKL-----NVCSIAKRN-PEAITEV-- 148
	: ::: : : : : :: : : : :
Db	159 VVDETDSLKRLDDFQRKLQELQKEKSDRLQKVLEFVSTVHDLCAVRLDFLSTVTEVHP 218

Qy	149 -----VQLPNHFSNRYYNRLVRSLLCDEDTVSTIRDSLMEKIGPNMASLFHILQT 199
	: :: : :: : :: : ::::
Db	219 SLDEANGVQTKS-ISNETLARLAKTVLTLKEDKMQRLLKK--LQELATQLTDLWNLMDT 273

RESULT 8
 Q91YR4
 ID Q91YR4 PRELIMINARY; PRT; 1108 AA.
 AC Q91YR4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to adaptor-related protein complex AP-3, beta 1 subunit.
GN AP3B1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC015068; AAH15068.1; -.
DR MGD; MGI:1333879; Ap3b1.
DR GO; GO:0008237; F:metallolopeptidase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002553; Adaptn_N.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01602; Adaptn_N; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 1108 AA; 123155 MW; 7B436C3E32C3E2E3 CRC64;

Query Match 7.3%; Score 92; DB 11; Length 1108;
Best Local Similarity 21.2%; Pred. No. 9;
Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLMSALQVGCGAFACL 60
:||: :|: :: | :||: | | :|| || :| : :
Db 307 LLQSRNAAVVMAVAQLYWH-----ISPKSE--AGVISKSLVRLRSNREVQYIVLQNI 357

Qy 61 ENSTCDTDGMYD-ICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFL----- 109
: : ||:: ||| | : | | | || :|| |
Db 358 ATMSIERKGMEPYLKSF-YVRSTDPTMIKTLKLEILTNLANEANISTLLREFQTYVRSQ 416

Qy 110 -----AIRRCSTFQRMIAEVQEECYSKLNVCIAKRNPAAITE---VVQLPNHFS 156
| ||:| |:|| : | : | || :: |: : | | :|:
Db 417 DKQFAAATIQTIGRCAT---SISEVTDTCLNGL-VCLLSNRDEIVVAESVVVIKKLLQMQ 472

Qy 157 NRYYNRLVRSILLE-CDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRAFDNRR 215
: ::| : : | || | || :|| | | : |
Db 473 PAQHGEIIRHMAKLLDSITVPVARASILWLIGEN-----CERVPKIA----- 514

Qy 216 TNEPQKLKVLLRNLRGEED 234
| |: : :: |:|
Db 515 ---PDVLRKMAKSFTSEDD 530

RESULT 9
Q8IHR6

ID Q8IHR6 PRELIMINARY; PRT; 1068 AA.
AC Q8IHR6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Coat protein, gamma subunit, putative.
GN PF11_0463.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014843; AAN36043.1; -.
DR InterPro; IPR002553; Adaptein_N.
DR InterPro; IPR008938; ARM.
DR Pfam; PF01602; Adaptein_N; 1.
SQ SEQUENCE 1068 AA; 124368 MW; 0710F427B066B12F CRC64;

Query Match 7.2%; Score 91.5; DB 5; Length 1068;
Best Local Similarity 22.3%; Pred. No. 9.6;
Matches 45; Conservative 31; Mismatches 53; Indels 73; Gaps 11;

Qy 37 QNSAEVVRCLNSALQVGCGAFACLENSTCDTDGYDICKSFLYSAAKFDTQGKAFVKESL 96
:| :: :| : :| .||||| ||||| : ||| |
Db 581 KNPSKYIRYIYNRL-----LLENSTIRIDGYM---ALFYIA-----L 614

Qy 97 KCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLN--VCSIAKRNPEAITEVVQLPN- 153
|| | || | : | ::|: :| : | : :: | | | |: |
Db 615 KCAEN---SKDILVLLNC----LLADNDDEVRDRTNFYYMLKEKIKELDTSNKQISNE 666

Qy 154 -----HFSNRYYNRLVRSLLCEDDEDTVSTIRDSEMEKIGPNMASLFHI 196
|:|| | |: ||| |::| |: |
Db 667 YEEKLQNNENINEHNNIHYSN---NNLIDQLLEYDQNT-----NIDQLLYF 709

Qy 197 LQTDHCAQTHPRADFNRRRTNE 218
: ::| : |: :| : |
Db 710 I-SNH-IEKDPKEEFSYQHVKE 729

RESULT 10

Q9GV74

ID Q9GV74 PRELIMINARY; PRT; 454 AA.
AC Q9GV74;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Differentiation associate-1.
GN DIA-1.

OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20347020; PubMed=10887082;
 RA Hirose S., Inazu Y., Chae S., Maeda Y.;
 RT "Suppression of the growth/differentiation transition in Dictyostelium development by transient expression of a novel gene, dial.";
 RL Development 127:3263-3270(2000).
 DR EMBL; AB007026; BAB13513.1; -.
 SQ SEQUENCE 454 AA; 48601 MW; 529D28B2D1908B85 CRC64;

 Query Match 7.1%; Score 90.5; DB 5; Length 454;
 Best Local Similarity 21.1%; Pred. No. 4.3;
 Matches 46; Conservative 42; Mismatches 93; Indels 37; Gaps 11;

 Qy 45 CLNSALQVCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGK---AFVKESLKCIA 100
 |||| | | :: :|| :|| | :|| | | :| ::|| :: | : :|
 Db 227 CLNGANGYSCKSY--VENQSCDPSDEYPVCNSD-YQSKCNSKGKGSCQSYYKLTQEC-- 281

 Qy 101 NGVTSKVFLAIRRCSTFQRMIAE----VQEECYSKLNVCASIARKNPEAITEVVQLPNHF 155
 ::|: | |: : | | | | :| | |: :: :| :| :: |
 Db 282 KDSSNKLVL----CAKSKNIPSYKDYVTQINCQSQL--CNYSR--DCIDPKAKVSTCF 332

 Qy 156 SN-----RYYNRLVRSLLCDEDVTSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRA 209
 :: | || | :| | | | | | :| :: :|:: :| :|
 Db 333 NDLFILMCPRYYQEPEIGSSSSSSSSSSGGSSNSNIFINIINIIIRSSE-SSNGSNS 391

 Qy 210 DFNRRRTNEPQKLKVLLRNLRGEEDSPSHIKRTSHESA 247
 : | :: | | | | | | | | | || ||:
 Db 392 NSVSSESSSPSSSSV-----ESSNSKSNHTSSESS 422

RESULT 11
 O14130
 ID O14130 PRELIMINARY; PRT; 783 AA.
 AC O14130;
 DT 01-JAN-1999 (TrEMBLrel. 09, Created)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative regulatory protein, zinc finger.
 GN SPAC3C7.04.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA Brown D., Churcher C.M.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA Wood V., Barrell B.G., Rajandream M.A.;

RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR CLUSTER
CC DOMAIN.
DR EMBL; Z99568; CAB16735.1; -.
DR PIR; T38690; T38690.
DR HSSP; P12351; 1HWT.
DR GeneDB_SPombe; SPAC3C7.04; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR007219; Fungal_trans.
DR InterPro; IPR001138; Fungi_TrN.
DR Pfam; PF04082; Fungal_trans; 1.
DR Pfam; PF00172; Zn_clus; 1.
DR SMART; SM00066; GAL4; 1.
DR PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.
DR PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Transcription;
KW Transcription regulation; Zinc.
SQ SEQUENCE 783 AA; 87957 MW; 4DD04F3865C448D2 CRC64;

Query Match 7.1%; Score 90.5; DB 3; Length 783;
Best Local Similarity 23.3%; Pred. No. 8.2;
Matches 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;

Qy 10 VLVISASATHEAEQNDSVSPRKSRRV-----AAQNSAEVVRCIQLNSALQVGCGAF----- 57
 :::| :| ||| |: ||| :| : |: | :|
Db 535 IIIMSRPVLLHKMKNAKNSPRVDRINEDCILAARHLISLVHLLQHSQLSCYSFFDNYT 594

Qy 58 -----ACLENSTCDTDGYMYDICKSFLYSAAKFDTQGKAFVKESLKCI----- 99
 |: |: | || : ||| : :| | | : |
Db 595 FSSALVVLLHCV-TEPCEED--DIAMQYAYSALDYMAEGNEAAKNCARVIRLFDAHLKG 650

Qy 100 ----ANGVTSKV-FLAIRRCSTFQRMIAEVQ-----EECYSKLNVCASIARKNPEAITEVV 149
 || ||: |:| :|| |||| |: | | | || ::|
Db 651 ARSDGNGNTSQSGFMA-----WQRWIAEVSAKDEPEKLMSPYNKSIGGGRNSNSLTPNA 704

Qy 150 QLPNHFSNRYYNR-----LVRSLLCEDEDTVSTIRDSLMEKIGPNMA---SLFHILQTD 200
 | | | :: | | |: | : :: | : | | ::| || : ||
Db 705 NLGADVS--FFPTDDTSFLLDHSKLDDLEKFASLDPI--KTPDLANDSSLLNWANTD 760

RESULT 12

Q8H2Y0

ID Q8H2Y0 PRELIMINARY; PRT; 622 AA.
AC Q8H2Y0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative transcription repressor HOTR.
GN OJ1113_E01.11.
OS *Oryza sativa* (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OJ1113_E01."
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP005437; BAC20898.1; -.
SQ SEQUENCE 622 AA; 68669 MW; 88302DE415DECDC9 CRC64;

Query Match 7.1%; Score 89.5; DB 10; Length 622;
Best Local Similarity 23.8%; Pred. No. 7.8;
Matches 41; Conservative 36; Mismatches 72; Indels 23; Gaps 8;

Qy 58 ACLENSTCDTDGMYDICKSFLYSAAKFDTQG--KAFVKESLKC-IANGVTSKVFLAIRRC 114
| :|: :| :||: | ||| : | || : || :: ||:
Db 415 APIEDGKQETSEVIDICE----AKKSDNSACTNKVISGSKCQLHNGCKAEEFVS--- 465

Qy 115 STFQRMIAEVQEECYSKLNVCIAKRNPPEAIT--EVVQLPNHFSNRYYNRLVRSLLECDE 172
| :| :| | | : :: | : | | : | | | : |:: |:
Db 466 ---SRVIDLLQNE--EKVKSMTVDKLSGEEISHGKYQSQENQPSGRMWFELIK--LQNPT 518

Qy 173 DTVSTIRDSLMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLKV 224
| :|: :| :|: | : | :| | | | : | :||:
Db 519 STLSSKGQGRQKRVTGNVAICEALTDNRCRETIPMA--GRERCDAHEGIKV 568

RESULT 13
O64605
ID O64605 PRELIMINARY; PRT; 1126 AA.
AC O64605;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F1707.15 protein.
GN F1707.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Oji O.,
RA Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
RA Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
RA Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
RA Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC F1707 sequence.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Theologis A.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC003671; AAC18813.1; -.
 DR PIR; T01491; T01491.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0006512; P:ubiquitin cycle; IEA.
 DR InterPro; IPR000569; HECT_domain.
 DR Pfam; PF00632; HECT; 1.
 DR SMART; SM00119; HECTc; 1.
 DR PROSITE; PS50237; HECT; 1.
 SQ SEQUENCE 1126 AA; 126148 MW; ODA1A3ACF6A8F64E CRC64;

Query Match 7.1%; Score 89.5; DB 10; Length 1126;
 Best Local Similarity 22.1%; Pred. No. 16;
 Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

Qy	14 SASATHEAEQNDSVSPRKSrvAAQNSAEVVRLNSALQVGCGAFACLENSTCD----- 66
	: : : : : :: :
Db	412 SSETQKDAESELVARRK-----NCAEL---YNIFLQLP-----QSDLCNLCMLLGY 455

Qy	67 ---TDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAE 123
	: : : : : : : : : : : : : : : :
Db	456 EGLSDKIYSLAGEVLKKLAAVDVTHRKFPTKELSELASGLSSSTVRVLATLSTTQKM--- 512

Qy	124 VQECCYSKLNVCASIARKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIR--- 179
	: : : : : : : : : : : : : : : :
Db	513 -----SQNTCSMA---GASILRVLQVLSSLTSTIDDNVGTDKETDQEEQNIMQGLKV 562

Qy	180 --DSLMEKIGPNMASLFHILQTDHCAQT 205
	: : : :: : : : : : : : :
Db	563 ALEPLWQELGQCIS--MTELQLDHTAAT 588

RESULT 14

Q9M7K6
 ID Q9M7K6 PRELIMINARY; PRT; 3658 AA.
 AC Q9M7K6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ubiquitin-protein ligase 2.
 GN UPL2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
 OC Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20040063; PubMed=10571878;
 RA Bates P.W., Vierstra R.D.;
 RT "UPL1 and 2, two 405 kDa ubiquitin-protein ligases from Arabidopsis
 thaliana related to the HECT-domain protein family.";
 RL Plant J. 20:183-195(1999).
 DR EMBL; AF127565; AAF36455.1; -.
 DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0006512; P:ubiquitin cycle; IEA.
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR000569; HECT_domain.
 DR InterPro; IPR000449; UBA_domain.
 DR InterPro; IPR003903; UIM.
 DR Pfam; PF00632; HECT; 1.
 DR Pfam; PF00627; UBA; 1.
 DR Pfam; PF02809; UIM; 1.
 DR SMART; SM00119; HECTc; 1.
 DR SMART; SM00165; UBA; 1.
 DR SMART; SM00726; UIM; 1.
 DR PROSITE; PS50237; HECT; 1.
 DR PROSITE; PS50030; UBA; 1.
 DR PROSITE; PS50330; UIM; 1.
 KW Ligase.
 SQ SEQUENCE 3658 AA; 403582 MW; 1FB4F8EB8C1F73D1 CRC64;

 Query Match 7.1%; Score 89.5; DB 10; Length 3658;
 Best Local Similarity 22.1%; Pred. No. 65;
 Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

 Qy 14 SASATHEAEQNDSVSPRKSRRVAAQNSAEVVRCILNSALQVGCGAFACLENSTCD----- 66
 |: :|| ||: || | ||: | ||: :: |:
 Db 2977 SSETQKDAESELSVARRK-----NCAEL--YNIFLQLP-----QSDLCNLCMLLGY 3020

 Qy 67 ---TDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAE 123
 :| :| : | | | | : | : | :|:|::| : | || |:
 Db 3021 EGLSDKIYSLAGEVLKKLAADVTHRKFETKELSELASGLSSSTVRVLATLSTTQKM--- 3077

 Qy 124 VQEECYSKLNVCASIARKRNPEAITEEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIR--- 179
 | ||:| :| | |:|: :| :|:|:|:|:|:|:|:
 Db 3078 -----SQNTCSMA---GASILRVLQVLSSLTSTIDDSNVGTDKETDQEEQNIMQGLKV 3127

 Qy 180 --DSLMEKIGPNMASLFHILQTDHCAQT 205
 :| ::| ::| || | | |
 Db 3128 ALEPLWQELGQCIS--MTELQLDHTAAT 3153

RESULT 15

Q8CP76
 ID Q8CP76 PRELIMINARY; PRT; 9439 AA.
 AC Q8CP76;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE EbhA protein.
 GN SE1128.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;

RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE016747; AAO04725.1; -.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR002988; GA.
DR Pfam; PF05738; Cna_B; 1.
DR Pfam; PF01468; GA; 39.
KW Complete proteome.
SQ SEQUENCE 9439 AA; 1050771 MW; 5A8C68E9AA31CDD4 CRC64;

Query Match 7.1%; Score 89.5; DB 16; Length 9439;
Best Local Similarity 22.0%; Pred. No. 2e+02;
Matches 50; Conservative 38; Mismatches 78; Indels 61; Gaps 11;

Qy 17 ATHEAEQ---NDSVSPRKS RVA-----AQNSAEVVRCLNSALQ 51
| :|||: || :|| :|| | :|| | :|| | :|| | :|| |
Db 2190 AKNEAERILGND--NPQVSQVTQALNKIKAIQPKLTEAINMLQNKENNTELVNAKRN--- 2244

Qy 52 VGCGAFACLENSTCDTDGMYDICKSFL--YSAAKFDTQGKAFVKE SLKCIANG----- 102
|||: ||| : : : : ||| | : | : : : : |||
Db 2245 -----LENAVNDTDPHTGMTQETINNNYNAKKREAQNE--IQKANMIINNGDATAQDI 2294

Qy 103 -----VTSKVFLAIRRCSTFQRMIAEVQE E CYSKL--NVCSI AKRNPEAITEVVQLPNHF 155
|| |:: | : | : ||| | : | : | : | : | : | : |
Db 2295 SSEKSKVEQVLQALQNAKNDLRADKRELQTAYNKLIQNVNTNGKK-PSSIQNYKSARRNI 2353

Qy 156 SNRY--YNRLVRSLL ECDED TVSTIRDSL--MEKIGPNMASLFHILQ 198
| :| ::|| ||: : ||| : | + : : |||
Db 2354 ENQYNTAKNEAHNVLENTNPTVNAVEDALRKINAIQPEVTKAINILQ 2400

Search completed: July 19, 2004, 15:33:30
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2004, 15:29:18 ; Search time 13 Seconds
(without alignments)
989.333 Million cell updates/sec

Title: US-10-614-990-2
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapext 0.5 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1268	100.0	247	1	STC1_HUMAN	P52823 homo sapien
2	1234	97.3	247	1	STC1_MOUSE	O55183 mus musculu
3	1231	97.1	247	1	STC1_RAT	P97574 rattus norv
4	682	53.8	250	1	STC_ANGAU	P18301 anguilla au
5	662.5	52.2	256	1	STC_ONCKI	Q08264 oncorhynchu
6	662.5	52.2	256	1	STC_ONCMY	P43648 oncorhynchu
7	617	48.7	179	1	STC_ONCKE	P43647 oncorhynchu
8	354.5	28.0	296	1	STC2_MOUSE	O88452 mus musculu
9	354	27.9	302	1	STC2_HUMAN	O76061 homo sapien
10	352	27.8	302	1	STC2_MACNE	O97561 macaca neme
11	349	27.5	296	1	STC2_RAT	Q9r0k8 rattus norv
12	181.5	14.3	197	1	STC2_CAVPO	P57675 cavia porce
13	156	12.3	40	1	STC_ONCNE	P43649 oncorhynchu
14	94	7.4	1105	1	A3B1_MOUSE	Q9z1t1 mus musculu
15	90.5	7.1	289	1	SNAAT_VITVI	P93798 vitis vinif
16	87.5	6.9	1465	1	DPOA_MOUSE	P33609 mus musculu
17	86.5	6.8	509	1	VP67_NPVCF	P41717 choristoneu

18	86	6.8	581	1	YMM7_YEAST	Q03124 saccharomyc
19	86	6.8	695	1	TRFL_HORSE	O77811 equus cabal
20	84.5	6.7	1451	1	DPOA_RAT	O89042 rattus norv
21	83	6.5	1094	1	A3B1_HUMAN	O00203 homo sapien
22	82.5	6.5	1483	1	UFD4_YEAST	P33202 saccharomyc
23	82.5	6.5	2335	1	TOR1_SCHPO	O14356 schizosacch
24	81.5	6.4	708	1	TRFL_BOVIN	P24627 bos taurus
25	81.5	6.4	804	1	S15A_HUMAN	Q8tag9 homo sapien
26	81	6.4	4377	1	ANK3_HUMAN	Q12955 homo sapien
27	80	6.3	509	1	VP64_NPVOP	P13625 orgyia pseu
28	80	6.3	851	1	STR8_MOUSE	Q8k031 mus musculu
29	80	6.3	998	1	ECA3_ARATH	Q9sy55 arabidopsis
30	79.5	6.3	609	1	MC70_YEAST	Q12411 saccharomyc
31	79.5	6.3	708	1	TRFL_BUBBU	O77698 bubalus bub
32	79	6.2	440	1	V117_FOWPV	Q9j5a5 fowlpox vir
33	78.5	6.2	132	1	IL4_HORSE	P42202 equus cabal
34	78.5	6.2	708	1	TRFL_CAPHI	Q29477 capra hircu
35	78.5	6.2	1127	1	MDM1_YEAST	Q01846 saccharomyc
36	78	6.2	458	1	IF3T_TORCA	P23729 torpedo cal
37	78	6.2	688	1	DNAK_ANAVA	O05714 anabaena va
38	78	6.2	803	1	GYRB_BUCAI	P57126 buchnera ap
39	78	6.2	1816	1	KF1B_MOUSE	Q60575 mus musculu
40	77.5	6.1	640	1	CLAT_MOUSE	Q03059. mus musculu
41	77	6.1	249	1	TPIS_TREPA	O83548 treponema p
42	77	6.1	1023	1	STR8_HUMAN	Q92502 homo sapien
43	76.5	6.0	229	1	Z313_MOUSE	Q9et26 mus musculu
44	76.5	6.0	455	1	TBA1_SCHPO	P04688 schizosacch
45	76	6.0	324	1	NAA2_RHILO	Q982f2 rhizobium l

ALIGNMENTS

RESULT 1

STC1_HUMAN
ID STC1_HUMAN STANDARD; PRT; 247.AA.
AC P52823;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Stanniocalcin 1 precursor (STC-1).
GN STC1 OR STC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibrosarcoma, and Lung carcinoma;
RX MEDLINE=96077825; PubMed=7489828;
RA Chang A.C.-M., Janosi J., Hulsbeek M., de Jong D., Jeffrey K.J.,
RA Noble J.R., Reddel R.R.;
RT "A novel human cDNA highly homologous to the fish hormone
stanniocalcin.";
RL Mol. Cell. Endocrinol. 112:241-247(1995).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Fetal lung;
RX MEDLINE=96312491; PubMed=8700837;
RA Olsen H.S., Cepeda M.A., Zhang Q.-Q., Rosen C.A., Vozzolo B.L.,
RA Wagner G.F.;
RT "Human stanniocalcin: a possible hormonal regulator of mineral
RT metabolism.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1792-1796(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Jeffrey K.J., Reddel R.R.;
RT "Characterization of the human stanniocalcin 1 gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, Kidney, and Stomach;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
CC therefore prevent hypercalcemia.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in most tissues, with the highest
CC levels in ovary, prostate, heart, kidney and thyroid. In the
CC kidney, expression is confined to the nephron, specifically in the
CC distal convoluted tubule and in the collecting tubule. Not
CC detected in the brain, liver, spleen, peripheral blood leukocytes
CC and adrenal medulla.
CC -!- SIMILARITY: Belongs to the stanniocalcin family.
CC -----
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CC -----
DR EMBL; U25997; AAC09472.1; -.

DR EMBL; U46768; AAA88903.1; -.
 DR EMBL; AF242179; AAL79522.1; -.
 DR EMBL; BC029044; AAH29044.1; -.
 DR Genew; HGNC:11373; STC1.
 DR MIM; 601185; -.
 DR GO; GO:0005181; F:glycopeptide hormone; TAS.
 DR GO; GO:0005180; F:peptide hormone; TAS.
 DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007584; P:response to nutrients; TAS.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT PROPEP 18 33 POTENTIAL.
 FT CHAIN 34 247 STANNIOCALCIN 1.
 FT DISULFID 45 59 BY SIMILARITY.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 65 114 BY SIMILARITY.
 FT DISULFID 98 128 BY SIMILARITY.
 FT DISULFID 135 170 BY SIMILARITY.
 FT DISULFID 202 202 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 247 AA; 27621 MW; 1E4A8BD861B49AED CRC64;

 Query Match 100.0%; Score 1268; DB 1; Length 247;
 Best Local Similarity 100.0%; Pred. No. 3.4e-102;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCILNSALQVGCGAFACL 60
 |||||||
 Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCILNSALQVGCGAFACL 60

 Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
 |||||||
 Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

 Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180
 |||||||
 Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180

 Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
 |||||||
 Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

 Qy 241 RTSHESA 247
 |||||
 Db 241 RTSHESA 247

RESULT 2
 STC1_MOUSE
 ID STC1_MOUSE STANDARD; PRT; 247 AA.
 AC O55183;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Stanniocalcin 1 precursor (STC-1).
GN STC1 OR STC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=97179050; PubMed=9027337;
RA Chang A.C.-M., Dunham M.A., Jeffrey K.J., Reddel R.R.;
RT "Molecular cloning and characterization of mouse stanniocalcin cDNA.";
RL Mol. Cell. Endocrinol. 124:185-187(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
therefore prevent hypercalcemia (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in many tissues.
CC -!- SIMILARITY: Belongs to the stanniocalcin family.
CC -----
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CC -----
DR EMBL; U47815; AAC00050.1; -.
DR EMBL; BC021425; AAH21425.1; -.
DR MGD; MGI:109131; Stc1.
DR GO; GO:0005615; C:extracellular space; IDA.
DR InterPro; IPR004978; Stanniocalcin.

DR Pfam; PF03298; Stanniocalcin; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT PROPEP 18 33 POTENTIAL.
 FT CHAIN 34 247 STANNIOCALCIN 1.
 FT DISULFID 45 59 BY SIMILARITY.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 65 114 BY SIMILARITY.
 FT DISULFID 98 128 BY SIMILARITY.
 FT DISULFID 135 170 BY SIMILARITY.
 FT DISULFID 202 202 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 247 AA; 27480 MW; DAD30D08575A513B CRC64;

Query Match 97.3%; Score 1234; DB 1; Length 247;
 Best Local Similarity 96.4%; Pred. No. 2.9e-99;
 Matches 238; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

 Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCALNSALQVGCGAFACL 60
 |||||||:|| | ||||:| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 MLQNSAVILALVISAAAHEAEQNDSVSPRKSRAAQNSAEVVRCALNSALQVGCGAFACL 60

 Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
 ||||||| ||||||| ||||||| ||||||| ||||||| :||| ||||||| |||||||
 Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 120

 Qy 121 IAEVQEECYSKLNVCSIAKRNPEAITEVQQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
 |||||||:||| ||||||| ||||||| ||||||| :||| ||||||| ||||||| |||||||
 Db 121 IAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

 Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEGDSPSHIK 240

 Qy 241 RTSHESA 247
 ||| |||
 Db 241 RTSQESA 247

RESULT 3

STC1_RAT
 ID STC1_RAT STANDARD PRT; 247 AA.
 AC P97574;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Stanniocalcin 1 precursor (STC-1).
 GN STC1 OR STC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RA Abe T., Tanemoto M., Hall A.E., Brown E.M., Hebert S.C.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
 CC therefore prevent hypercalcemia (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the stanniocalcin family.
 CC -----
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 CC -----
 DR EMBL; U62667; AAB39541.1; -.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT PROPEP 18 33 POTENTIAL.
 FT CHAIN 34 247 STANNIOCALCIN 1.
 FT DISULFID 45 59 BY SIMILARITY.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 65 114 BY SIMILARITY.
 FT DISULFID 98 128 BY SIMILARITY.
 FT DISULFID 135 170 BY SIMILARITY.
 FT DISULFID 202 202 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 247 AA; 27507 MW; DAC2FD08575A513B CRC64;

 Query Match 97.1%; Score 1231; DB 1; Length 247;
 Best Local Similarity 96.0%; Pred. No. 5.2e-99;
 Matches 237; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

 QY 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRSRVAAQNSAEVVRCNSALQVGCGAFACL 60
 |||||||:| |||||:| |||||||||||||||||||||||||||||||||||||||
 Db 1 MLQNSAVILALVISAAAHEAEQNDSVSPRSRVAAQNSAEVVRCNSALQVGCGAFACL 60

 QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
 |||||||||||||||||||||||||||||||:|||||||||||||||||
 Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 120

 QY 121 IAEVQEECYSKLNVCSTIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180
 |||||||:|||||||||||||||||:|||||||||||||||||||||
 Db 121 IAEVQEDCYSKLNVCSTIARKNPEAITEVIQLPNHFSNRYYNRLVRSLLCEDDETVSTIRD 180

 Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEDSPSHIK 240
 |||||||:|||||||||||||||||:|||||||||||||||||
 Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEGDSPSHIK 240

 Qy 241 RTSHESA 247
 ||| :|:
 Db 241 RTSQENA 247

RESULT 4
 STC_ANGAU

ID STC_ANGAU STANDARD; PRT; 250 AA.

AC P18301;

DT 01-NOV-1990 (Rel. 16, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Stanniocalcin precursor (STC) (Corpuscles of stannius protein) (CS)

DE (Hypocalcin) (Teleocalcin).

GN STC.

OS Anguilla australis (Australian eel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;

OC Anguilla.

OX NCBI_TaxID=7940;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 33-57.

RX MEDLINE=88083961; PubMed=3319739;

RA Butkus A., Roche P.J., Fernley R.T., Haralambidis J.,

RA Penschow J.D., Ryan G.B., Trahair J.F., Tregear G.W., Coghlan J.P.;

RT "Purification and cloning of a corpuscles of Stannius protein from

RT Anguilla australis.";

RL Mol. Cell. Endocrinol. 54:123-133(1987).

RN [2]

RP REVISIONS.

RA Roche P.J.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Its primary function is the prevention of hypercalcemia.

CC Upon release into the circulation, it lowers calcium transport by

CC the gills, thereby reducing its rate of influx from the

CC environment into the extracellular compartment. STC also

CC stimulates phosphate reabsorption by renal proximal tubules. The

CC consequence of this action is increased levels of plasma

CC phosphate, which combines with excess calcium and promotes its

CC disposal into bone and scales.

CC -!- SUBUNIT: Homodimer; disulfide-linked.

CC -!- TISSUE SPECIFICITY: Corpuscles of Stannius.

CC -!- SIMILARITY: Belongs to the stanniocalcin family.

CC -----

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CC -----

DR EMBL; M36967; AAB91483.1; -.

DR PIR; A54648; A54648.

DR InterPro; IPR004978; Stanniocalcin.

DR Pfam; PF03298; Stanniocalcin; 1.

KW Hormone; Signal; Glycoprotein.

FT SIGNAL 1 17 POTENTIAL.

FT PROPEP 18 32 POTENTIAL.

FT CHAIN 33 250 STANNIOCALCIN.

FT DISULFID 44 58 BY SIMILARITY.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 64 113 BY SIMILARITY.

FT DISULFID 97 127 BY SIMILARITY.

FT DISULFID 134 169 BY SIMILARITY.
 FT DISULFID 201 201 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC . . .) (PROBABLE).
 SQ SEQUENCE 250 AA; 27174 MW; BB972BD951F75B3E CRC64;

 Query Match 53.8%; Score 682; DB 1; Length 250;
 Best Local Similarity 54.3%; Pred. No. 1.1e-51;
 Matches 138; Conservative 47; Mismatches 57; Indels 12; Gaps 6;

 Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRSRVAQQNSAEVVRCLNSALQVGCGAFACL 60
 ||: | ::| ||: :| :| :::: :||| :| :| : ::| ||||| ||||||| |||||
 Db 1 MLRMSGILTLVLTAAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFACL 59

 Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRM 120
 :||||:||||:|||:|||: ||||||| ||||||| |||||||:||||:|||:
 Db 60 DNSTCNDGMHEICRSFLHGAAKFDTQGKTFVKESLKCIAANGITSKVFLTIRRCSSFQKM 119

 Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
 |:|||||:|||:|||:|: ||||: ||| :|: | |||: |:||||| ||||||| :|
 Db 120 ISEVQEECYSKLDLCSVQAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLTCDEDTVEQVRA 179

 Qy 181 SLMEKIGPNMASLFHILQTDHC----AQTHP-RADFNRRTNEPQKLKVLLRNLRGEED 234
 |: :: | | || :||| | | | | | : | | | | :| | | | :| | | | :|
 Db 180 GLVSRLEPEMGVLFQLLQTAKACPPSAAGGTGPVGAGGSWRWPMGPPMFKI-QPNLRSRD- 237

 Qy 235 SPSHI--KRTSHES 246
 |:|: |: | |
 Db 238 -PTHLFAKKRSTSS 250

RESULT 5
 STC_ONCKI
 ID STC_ONCKI STANDARD; PRT; 256 AA.
 AC Q08264;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Stanniocalcin precursor (STC) (Corpuscles of stannius protein) (CS)
 DE (Hypocalcin) (Teleocalcin).
 GN STC.
 OS Oncorhynchus kisutch (Coho salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8019;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93246046; PubMed=1363790;
 RA Wagner G.F., Dimattia G.E., Davie J.R., Copp D.H., Friesen H.G.;
 RT "Molecular cloning and cDNA sequence analysis of coho salmon
 stanniocalcin.";
 RL Mol. Cell. Endocrinol. 90:7-15(1992).
 RN [2]
 RP SEQUENCE OF 34-73.
 RX MEDLINE=89065334; PubMed=3197944;
 RA Wagner G.F., Fenwick J.C., Park C.M., Milliken C., Copp D.H.,
 Friesen H.G.;

RT "Comparative biochemistry and physiology of teleocalcin from sockeye
RT and coho salmon.";
RL Gen. Comp. Endocrinol. 72:237-246(1988).
CC -!- FUNCTION: Its primary function is the prevention of hypercalcemia.
CC Upon release into the circulation, it lowers calcium transport by
CC the gills, thereby reducing its rate of influx from the
CC environment into the extracellular compartment. STC also
CC stimulates phosphate reabsorption by renal proximal tubules. The
CC consequence of this action is increased levels of plasma
CC phosphate, which combines with excess calcium and promotes its
CC disposal into bone and scales.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of
CC stannius.
CC -!- SIMILARITY: Belongs to the stanniocalcin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S59519; AAB26419.1; -.
DR PIR; B60841; B60841.
DR PIR; I51197; I51197.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Hormone; Signal; Glycoprotein; Calcium transport.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 33 BY SIMILARITY.
FT CHAIN 34 256 STANNIOCALCIN.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 256 AA; 28074 MW; E688B930B394A8D3 CRC64;

Query Match 52.2%; Score 662.5; DB 1; Length 256;
Best Local Similarity 53.4%; Pred. No. 5.3e-50;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

Qy 11 LVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCCLNSALQVGCGAFACLENSTCDTDGM 70
||: :|| : : :: ||||::| : : : |||| || |||| | ||||| ||||||| |||||
Db 12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
:||||: | :||| |:||||| |||||||:||||| ||||| | |||||:|||||
Db 71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVQTIRRCGVFQRMISEVQEECYS 130

Qy 131 KLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRDSLMEKIGPNM 190
:||:| :|: ||||| ||||:| || ||||: ||:||| ||||:||: |: |: :||:|:
Db 131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPD 190

Qy 191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
:|| :|| . || | : : | | | |: :|| : |:|:
Db 191 ETLFQLLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241

RESULT 6

STC_ONCMY

ID STC_ONCMY STANDARD; PRT; 256 AA.

AC P43648; Q98SE1;

DT 01-NOV-1995 (Rel. 32, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Stanniocalcin precursor (STC) (Corpuscles of stannius protein) (CS)

DE (Hypocalcin) (Teleocalcin).

GN STC.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RA McCudden C.R., Wagner G.F.;

RT "Rainbow trout ovarian stanniocalcin.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 34-66.

RC TISSUE=Stannius corpuscles;

RX MEDLINE=88196801; PubMed=3360288;

RA Lafeber F.P.J.G., Hanssen R.G.J.M., Choy Y.M., Flik G.,

RA Herrmann-Erlee M.P.M., Pang P.K.T., Wendelaar Bonga S.E.;

RT "Identification of hypocalcin (teleocalcin) isolated from trout

RT Stannius corpuscles.";

RL Gen. Comp. Endocrinol. 69:19-30(1988).

CC --!- FUNCTION: Its primary function is the prevention of hypercalcemia.

CC Upon release into the circulation, it lowers calcium transport by

CC the gills, thereby reducing its rate of influx from the

CC environment into the extracellular compartment. STC also

CC stimulates phosphate reabsorption by renal proximal tubules. The

CC consequence of this action is increased levels of plasma

CC phosphate, which combines with excess calcium and promotes its

CC disposal into bone and scales.

CC --!- SUBUNIT: Homodimer; disulfide-linked.

CC --!- SUBCELLULAR LOCATION: Secreted.

CC --!- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of

CC stannius.

CC --!- SIMILARITY: Belongs to the stanniocalcin family.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF326317; AAK01423.1; -.

DR EMBL; AF326318; AAK01424.1; -.

DR InterPro; IPR004978; Stanniocalcin.

DR Pfam; PF03298; Stanniocalcin; 1.

KW Hormone; Signal; Glycoprotein; Calcium transport.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 33
 FT CHAIN 34 256 STANNIocalcin.
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. .).
 FT VARIANT 41 41 D -> E.
 SQ SEQUENCE 256 AA; 28104 MW; E688A0E0B394A8D3 CRC64;

 Query Match 52.2%; Score 662.5; DB 1; Length 256;
 Best Local Similarity 53.4%; Pred. No. 5.3e-50;
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

 Qy 11 LVISASATHEAEQNDSVSPRSRVAQNSAEVVRCLNSALQVGCGAFACLENSTCDTG 70
 ||: :|| : : :: ||::| : : ::| |||| | |||| ||||||| |||||
 Db 12 LVLGTAATFDTPPEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTG 70

 Qy 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFORMIAEVQEECYS 130
 :||: | ::|| |:|||| ||||||:|||||:|||||:||||| |||| | ||||:|||||
 Db 71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFTIRRCGVFQRMISEVQEECYS 130

 Qy 131 KLNVCSTIAKRNPAAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRDLSLMEKIGPNM 190
 :||:| :|: ||||| ||||:| || ||||:| :||| ||||:||: :| |: ::||:|
 Db 131 RLDICGVARSNPEAIGEVVQVPAHFNPNEYSTLLQSLLACDEETVAVVRAGLVARLGPM 190

 Qy 191 ASLFHILQTDHCAQTHPRADFN----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
 :|| :|| || | : : | | | :|| :| :|| :|:
 Db 191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241

RESULT 7

STC_ONCKE
 ID STC_ONCKE STANDARD; PRT; 179 AA.
 AC P43647; Q91427;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Stanniocalcin (STC) (Corpuscles of stannius protein) (CS) (Hypocalcin)
 DE (Teleocalcin).
 GN STC.
 OS Oncorhynchus keta (Chum salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8018;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE.
 RC TISSUE=Stannius corpuscles;
 RX MEDLINE=96077816; PubMed=7489819;
 RA Yamashita K., Koide Y., Itoh H., Kawada N., Kawauchi H.;
 RT "The complete amino acid sequence of chum salmon stanniocalcin, a
 calcium-regulating hormone in teleosts.";
 RL Mol. Cell. Endocrinol. 112:159-167(1995).
 RN [2]
 RP SEQUENCE OF 1-33.
 RC TISSUE=Stannius corpuscles;
 RX MEDLINE=93055697; PubMed=1430418;
 RA Sundell K., Bjoernsson B.T., Itoh H., Kawauchi H.;

RT "Chum salmon (*Oncorhynchus keta*) stanniocalcin inhibits in vitro
RT intestinal calcium uptake in Atlantic cod (*Gadus morhua*).";
RL J. Comp. Physiol. B 162:489-495(1992).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=99216273; PubMed=10198206;
RA Hulova I., Kawauchi H.;
RT "Assignment of disulfide linkages in chum salmon stanniocalcin.";
RL Biochem. Biophys. Res. Commun. 257:295-299(1999).
CC -!-- FUNCTION: Its primary function is the prevention of hypercalcemia.
CC Upon release into the circulation, it lowers calcium transport by
CC the gills, thereby reducing its rate of influx from the
CC environment into the extracellular compartment. STC also
CC stimulates phosphate reabsorption by renal proximal tubules. The
CC consequence of this action is increased levels of plasma
CC phosphate, which combines with excess calcium and promotes its
CC disposal into bone and scales.
CC -!-- SUBUNIT: Homodimer; disulfide-linked.
CC -!-- SUBCELLULAR LOCATION: Secreted.
CC -!-- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of
CC stannius.
CC -!-- SIMILARITY: Belongs to the stanniocalcin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S80134; AAB35648.2; --.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Hormone; Glycoprotein; Calcium transport.
FT DISULFID 12 26
FT DISULFID 21 41
FT DISULFID 32 81
FT DISULFID 65 95
FT DISULFID 102 137
FT DISULFID 169 169 INTERCHAIN.
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .).
FT CONFLICT 160 160 P -> L (IN REF. 1; AA SEQUENCE).
FT CONFLICT 170 170 S -> P (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 179 AA; 19518 MW; 0298CAC33E2BE445 CRC64;

Query Match 48.7%; Score 617; DB 1; Length 179;
Best Local Similarity 66.1%; Pred. No. 2.9e-46;
Matches 109; Conservative 28; Mismatches 28; Indels 0; Gaps 0;

Qy 40 AEVVRCLNSALQVGCGAFACLENSTCDTDGYDICKSFLYSAAKFDTQGKAFVKESLKCI 99
::| ||||. || |||| |||||||||:|||: | :|| |:||| |||||:|||
Db 7 SDVARCLNGALDVCGTFACLENSTCDGMHDICQLFFHTATFNTQGKTFVKESLRCI 66

Qy 100 ANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRY 159
||||||| |||| | |||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 67 ANGVTSKVFQTIRRCGVFQRMISEVQEECYSRLDICGVARSNPEAIGEVVQVPAHFPNRY 126

QY 160 YNRLVRSLLCDEDVTSTIRDSLMEKIGPNMASLFHILQTDHCAQ 204
| : | :: || | || | : || : | : | : || | : | : |
Db 127 YSTLLQSLLACDEETVAVVRAGLVARLGPDMETPFQQLQNKHCSQ 171

RESULT 8

STC2_MOUSE

ID STC2_MOUSE STANDARD; PRT; 296 AA.
AC O88452;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Stanniocalcin 2 precursor (STC-2).
GN STC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98389283; PubMed=9723890;
RA Chang A.C.-M., Reddel R.R.;
RT "Identification of a second stanniocalcin cDNA in mouse and human:
RT stanniocalcin 2.";
RL Mol. Cell. Endocrinol. 141:95-99(1998).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Breast carcinoma;
RX MEDLINE=99378040; PubMed=10450831;
RA Moore E.E., Kuéstner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA Buddle M.M., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT "Stanniocalcin 2: characterization of the protein and its localization
RT to human pancreatic alpha cells.";
RL Horm. Metab. Res. 31:406-414(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Has an anti-hypocalcemic action on calcium and phosphate
 CC homeostasis.
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- TISSUE SPECIFICITY: Found in a variety of tissues including
 CC skeletal muscle, small intestine, kidney, liver and brain.
 CC -!- SIMILARITY: Belongs to the stanniocalcin family.
 CC -----
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 CC -----
 DR EMBL; AF056244; AAC27507.1; -.
 DR EMBL; AF031035; AAD01921.1; -.
 DR EMBL; BC012206; AAH12206.1; -.
 DR MGD; MGI:1316731; Stc2.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 296 STANNIOCALCIN 2.
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 296 AA; 32601 MW; OC1EF4008912DE68 CRC64;

Query Match 28.0%; Score 354.5; DB 1; Length 296;
 Best Local Similarity 31.7%; Pred. No. 2.2e-23;
 Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

QY	7 VLLVLVISASATHEAEQNDSVSP-----RKSrvaaQNSAEVVRCLNSALQVGCGA 56
	: : : : : : : : : : : : : :
Db	10 VTLALVF--ATLDPAQGTDSTNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGC GV 67
	: : : : : : : : : : : : : :
QY	57 FACLENSTCDTDGYMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCST 116
	: : : : : : : : : : : : : :
Db	68 FECFENNNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKGFCISRKCPA 127
	: : : : : : : : : : : : : :
QY	117 FQRMIAEVQECCYSKLNVCASIARKNPEAITEEVVQLPNHFSNRYYNRLVRSLL ECDED TVS 176
	: : : : : : : : : : : : : : :
Db	128 IREMVFQLQRECYLKHDLC SAAQENVGVIVEMIFKD LLLLHEPYVDLVNLLTCGEDVKE 187
	: : : : : : : : : : : : : : :
QY	177 TIRDSLMEKIGPNMASLFHIL-----QTDHCAQTH---PRADFNRRRTNEPQLKV 224
	: : : : : : : : : : : : : : :
Db	188 AVTRSVQAQCEQS WGG LCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHHR DTDHHLT 247
	: : : : : : : : : : : : : : :
QY	225 LLRNLRGEDSPSHIK----RTSHESA 247
	: : : : : : : : : : : : : :
Db	248 ANRGAKGERGSKSHPN A HARGRTGGQSA 275

STC2_HUMAN
ID STC2_HUMAN STANDARD; PRT; 302 AA.
AC 076061;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Stanniocalcin 2 precursor (STC-2) (Stanniocalcin-related protein)
DE (STCRP) (STC-related protein).
GN STC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98389283; PubMed=9723890;
RA Chang A.C.-M., Reddel R.R.;
RT "Identification of a second stanniocalcin cDNA in mouse and human:
RT stanniocalcin 2.";
RL Mol. Cell. Endocrinol. 141:95-99(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Osteosarcoma;
RX MEDLINE=98440784; PubMed=9753616;
RA Ishiabshi K., Miyamoto K., Taketani Y., Morita K., Takeda E.,
RA Sasaki S., Imai M.;
RT "Molecular cloning of a second human stanniocalcin homologue (STC2).";
RL Biochem. Biophys. Res. Commun. 250:252-258(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99145369; PubMed=10022771;
RA DiMattia G.E., Varghese R., Wagner G.F.;
RT "Molecular cloning and characterization of stanniocalcin-related
RT protein.";
RL Mol. Cell. Endocrinol. 146:137-140(1998).
RN [4]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Breast carcinoma;
RX MEDLINE=99378040; PubMed=10450831;
RA Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA Buddle M.M., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT "Stanniocalcin 2: characterization of the protein and its localization
RT to human pancreatic alpha cells.";
RL Horm. Metab. Res. 31:406-414(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Has an anti-hypocalcemic action on calcium and phosphate
CC homeostasis.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues including
CC muscle, heart, pancreas, kidney, spleen, prostate, small
CC intestine, colon and peripheral blood Leucocytes.
CC -!- SIMILARITY: Belongs to the stanniocalcin family.
CC -----
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CC -----
DR EMBL; AF055460; AAC27036.1; -.
DR EMBL; AB012664; BAA33489.1; -.
DR EMBL; AF098462; AAC97948.1; -.
DR EMBL; AF031036; AAD01922.1; -.
DR EMBL; BC000658; AAH00658.1; -.
DR EMBL; BC006352; AAH06352.1; -.
DR EMBL; BC013958; AAH13958.1; -.
DR PIR; JE0357; JE0357.
DR Genew; HGNC:11374; STC2.
DR MIM; 603665; -.
DR GO; GO:0005181; F:glycopeptide hormone; TAS.
DR GO; GO:0005180; F:peptide hormone; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007584; P:response to nutrients; TAS.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 302 STANNIOCALCIN 2.
FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 302 AA; 33248 MW; 9B90D8911524FA22 CRC64;

Query Match 27.9%; Score 354; DB 1; Length 302;
Best Local Similarity 32.4%; Pred. No. 2.5e-23;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKSRRVAAQNSAEVVRCI NSALQVGCGAFACL 60

| | |::: | |: | | | | :| |:: | |:||: | | | | | |
Db 12 LALVLATFDPARGT DATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVCGVFECE 71

QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
| |::|: | :: | | :||:| | | | | | :| | | | | | | | | |
Db 72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKKAHALRHRFGCISRKCPAIREM 131

QY 121 IAEVQEECYSKLNVCISIARKRNPEAITEVVQLPNHFSNRYNRLVRSLL ECDEDTVSTIRD 180
| |::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132 VSQLORECYLKHDLCAAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLTCGEEVKEAITH 191

QY 181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQL----- 222
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251

QY 223 KVLLRNLRGEDSPSH 238
| : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 252 RETGRGAKGERGSKSH 267

RESULT 10

STC2_MACNE

ID STC2_MACNE STANDARD; PRT; 302 AA.
AC 097561;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Stanniocalcin 2 precursor (STC-2).
GN STC2.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreatic islets;
RX MEDLINE=99378040; PubMed=10450831;
RA Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA Buddle M.M., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT "Stanniocalcin 2: characterization of the protein and its localization
to human pancreatic alpha cells.";
RL Horm. Metab. Res. 31:406-414(1999).
CC -!- FUNCTION: Has an anti-hypocalcemic action on calcium and phosphate
CC homeostasis.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the stanniocalcin family.
CC -----
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CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; AF035377; AAD02027.1; -.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 302 STANNIOCALCIN 2.
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 302 AA; 33281 MW; 62953CE958AF64C1 CRC64;

Query Match 27.8%; Score 352; DB 1; Length 302;
 Best Local Similarity 32.8%; Pred. No. 3.7e-23;
 Matches 84; Conservative 44; Mismatches 102; Indels 26; Gaps 5;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKSRSVAAQNSAEVVRCILNSALQVGCGAFACL 60
 | ||:: ||: | | | :| |:: ||::||: || :| |||| | |
 Db 12 LALVLATIDPARGTDATNPPEGPQDRSSQQKGRSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
 ||::|: |::| | :|::| | | | ||::|:|:|:| |: : | :| : |
 Db 72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALCKCAHALRHRFGCISRKCPIREM 131

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
 : ::| | || | ::|: | :| | | |:: : | | || | | :| |
 Db 132 VFQLQRECYLKHDLCAAAQENTRIVEMIHFKDLLLHEPYVDLVNLTCGEEVKEATH 191

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHP-----RADFNRRRTNE----PQ-KL 222
 |: : | | || | | | | | | | | | | | | | | | | |:
 Db 192 SVQVQCEQNWGSLCSILSFCTSAIQRPPPTAPPERQPQVDRAKLSRAHHGEAHHLPEPSS 251

Qy 223 KVLLRNLRGEEDSPSH 238
 : | :|| | ||
 Db 252 RETGRGAKGERGSKSH 267

RESULT 11

STC2_RAT

ID STC2_RAT STANDARD; PRT; 296 AA.

AC Q9R0K8;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Stanniocalcin 2 precursor (STC-2).

GN STC2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=99439722; PubMed=10508929;

RA Honda S., Kashiwagi M., Ookata K., Tojo A., Hirose S. ;

RT "Regulation by lalpha,25-dihydroxyvitamin D(3) of expression of
 stanniocalcin messages in the rat kidney and ovary." ;

RL FEBS Lett. 459:119-122(1999).

CC !- FUNCTION: Has an anti-hypocalcemic action on calcium and phosphate

CC homeostasis.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues. Strongly
CC expressed in ovary and to a lesser extent in kidney.
CC -!- SIMILARITY: Belongs to the stanniocalcin family.
CC -----
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CC -----
DR EMBL; AB030707; BAA85251.1; -.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 296 STANNIOCALCIN 2.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 296 AA; 32621 MW; 0903639858D9B2DC CRC64;

Query Match 27.5%; Score 349; DB 1; Length 296;
Best Local Similarity 31.8%; Pred. No. 6.6e-23;
Matches 81; Conservative 44; Mismatches 106; Indels 24; Gaps 4;

RESULT 12

STC2_CAVPO
ID STC2_CAVPO STANDARD; PRT; 197 AA.
AC P57675;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Stannio calcin 2 (STC-2) (Fragments).

GN STC2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RX MEDLINE=99378040; PubMed=10450831;
RA Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA Buddle M.M., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT "Stanniocalcin 2: characterization of the protein and its localization
RT to human pancreatic alpha cells.";
RL Horm. Metab. Res. 31:406-414(1999).
CC -!- FUNCTION: Has an anti-hypocalcemic action on calcium and phosphate
CC homeostasis.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the stanniocalcin family.
KW Hormone.
FT NON_CONS 60 61
FT NON_CONS 64 65
FT NON_CONS 69 70
FT NON_CONS 75 76
FT NON_CONS 92 93
FT NON_CONS 154 155
SQ SEQUENCE 197 AA; 21899 MW; 1512DA859C8A8E67 CRC64;

Query Match 14.3%; Score 181.5; DB 1; Length 197;
Best Local Similarity 25.8%; Pred. No. 1.1e-08;
Matches 58; Conservative 27; Mismatches 85; Indels 55; Gaps 6;

Qy 25 DSVSPRKSRAAQNSAEVVRCLN SALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKF 84
| | :| ::||:||:|| :| || || || ||:| :| :|
Db 12 DRGSQQKGRLSLQNTAEIQHCLVNAGDVCGVFECFENNXCIXXLHXI----- 60

Qy 85 DTQGKAFVKE SLKCIANGVTSKVFLAIRRCSTFQRMIAEVQE E CYSKLN VCSI AKRN PEA 144
:|:| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 61 -----SFIKAH-----ALRFGCISREMVFQLQRECYLKHDLCMINFR--- 97

Qy 145 ITEVVQLPNHFSNRYYNRLVRSLL ECDED TVSTIRDSLMEKIGPNMASLFHIL----QT 199
: :| || || | :| :| :| :| :| :| :| :| :|
Db 98 -----DLLLHEPYVDLVNLLLTCGEDVKEAVTRSIQAQCEQNWGGLCSILSFCTS NV 149

Qy 200 DHCAQTHPRADFNRRTNEP-----QKLKVLLRNLRGEEDSPSH 238
| || | :| :| :| :| :| :| :| :| :|
Db 150 QRPXAXQPXAD--RAQVSRPHHDTGHHLLEAIXGAKGERGSKSH 192

RESULT 13
STC_ONCNE
ID STC_ONCNE STANDARD; PRT; 40 AA.
AC P43649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Stanniocalcin (STC) (Corpuscles of stannius protein) (CS) (Hypocalcin)

DE (Teleocalcin) (Fragment).
 GN STC.
 OS Oncorhynchus nerka (Sockeye salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8023;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89065334; PubMed=3197944;
 RA Wagner G.F., Fenwick J.C., Park C.M., Milliken C., Copp D.H.,
 RA Friesen H.G.;
 RT "Comparative biochemistry and physiology of teleocalcin from sockeye
 RT and coho salmon.";
 RL Gen. Comp. Endocrinol. 72:237-246(1988).
 CC -!- FUNCTION: Its primary function is the prevention of hypercalcemia.
 CC Upon release into the circulation, it lowers calcium transport by
 CC the gills, thereby reducing its rate of influx from the
 CC environment into the extracellular compartment. STC also
 CC stimulates phosphate reabsorption by renal proximal tubules. The
 CC consequence of this action is increased levels of plasma
 CC phosphate, which combines with excess calcium and promotes its
 CC disposal into bone and scales.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of
 CC stannius.
 CC -!- SIMILARITY: Belongs to the stanniocalcin family.
 DR PIR; A60841; A60841.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 KW Hormone; Glycoprotein; Calcium transport.
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. .).
 FT UNSURE 29 29
 FT NON_TER 40 40
 SQ SEQUENCE 40 AA; 4134 MW; 0C517B7BBC5EE6C CRC64;

 Query Match 12.3%; Score 156; DB 1; Length 40;
 Best Local Similarity 79.4%; Pred. No. 2.5e-07;
 Matches 27; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

 Qy 40 AEVVRCLNSAIVQVGCGAFACLENSTCDTDGMYDI 73
 ::| |||| | | | ||| ||||||| ||| :|||
 Db 7 SDVARCLNGALDVGCCTFACLENSTCDTDGMHDI 40

RESULT 14
 A3B1_MOUSE
 ID A3B1_MOUSE STANDARD; PRT; 1105 AA.
 AC Q9Z1T1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adapter-related protein complex 3 beta 1 subunit (Beta-adaptin 3A)
 DE (AP-3 complex beta-3A subunit) (Beta-3A-adaptin).
 GN AP3B1.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ;
RX MEDLINE=99135912; PubMed=9931340;
RA Feng L., Seymour A.B., Jiang S.Y., To A., Peden A.A., Novak E.K.,
RA Zhen L., Rusiniak M.E., Eicher E.M., Robinson M.S., Gorin M.B.,
RA Swank R.T.;
RT "The beta-3A subunit gene (Ap3b1) of the AP-3 adaptor complex is
RT altered in the mouse hypopigmentation mutant pearl, a model for
RT Hermansky-Pudlak syndrome and night blindness.";
RL Hum. Mol. Genet. 8:323-330(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=20512043; PubMed=11056055;
RA Feng L., Rigatti B.W., Novak E.K., Gorin M.B., Swank R.T.;
RT "Genomic structure of the mouse ap3b1 gene in normal and pearl mice.";
RL Genomics 69:370-379(2000).
CC -!- FUNCTION: Part of the AP-3 complex, an adaptor-related complex
CC which is not clathrin-associated. The complex is associated with
CC the Golgi region as well as more peripheral structures. It
CC facilitates the budding of vesicles from the Golgi membrane and
CC may be directly involved in trafficking to lysosomes.
CC -!- SUBUNIT: Assembly protein complex 3 (AP-3) is a heterotetramer
CC composed of two large chains (delta and beta3), a medium chain
CC (mu3) and a small chain (sigma3).
CC -!- PTM: Phosphorylated on serine residues (By similarity).
CC -!- DISEASE: Defects in AP3B1 are the cause of the autosomal recessive
CC phenotype 'pearl' (pe). Pearl mice exhibit hypopigmentation,
CC lysosomal secretion abnormalities, and platelet-dense granules
CC with reduced levels of adenine nucleotides and serotonin. The
CC changes in platelets lead to prolonged bleeding. Additionally,
CC pearl mice exhibit reduced sensitivity in the dark-adapted state.
CC -!- SIMILARITY: Belongs to the adaptor complexes large subunit
CC family.
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CC -----
DR EMBL; AF103809; AAC78338.1; -.
DR EMBL; AF255589; AAG23622.1; -.
DR EMBL; AF255566; AAG23622.1; JOINED.
DR EMBL; AF255567; AAG23622.1; JOINED.
DR EMBL; AF255568; AAG23622.1; JOINED.
DR EMBL; AF255569; AAG23622.1; JOINED.
DR EMBL; AF255570; AAG23622.1; JOINED.
DR EMBL; AF255571; AAG23622.1; JOINED.
DR EMBL; AF255572; AAG23622.1; JOINED.
DR EMBL; AF255573; AAG23622.1; JOINED.

DR EMBL; AF255574; AAG23622.1; JOINED.
DR EMBL; AF255575; AAG23622.1; JOINED.
DR EMBL; AF255576; AAG23622.1; JOINED.
DR EMBL; AF255577; AAG23622.1; JOINED.
DR EMBL; AF255578; AAG23622.1; JOINED.
DR EMBL; AF255579; AAG23622.1; JOINED.
DR EMBL; AF255580; AAG23622.1; JOINED.
DR EMBL; AF255581; AAG23622.1; JOINED.
DR EMBL; AF255582; AAG23622.1; JOINED.
DR EMBL; AF255583; AAG23622.1; JOINED.
DR EMBL; AF255584; AAG23622.1; JOINED.
DR EMBL; AF255585; AAG23622.1; JOINED.
DR EMBL; AF255586; AAG23622.1; JOINED.
DR EMBL; AF255587; AAG23622.1; JOINED.
DR EMBL; AF255588; AAG23622.1; JOINED.
DR PIR; T18295; T18295.
DR MGD; MGI:1333879; Ap3b1.
DR InterPro; IPR002553; Adaptein_N.
DR InterPro; IPR008938; ARM.
DR Pfam; PF01602; Adaptein_N; 1.
KW Golgi stack; Protein transport; Transport; Phosphorylation.
FT DOMAIN 678 802 GLU/SER-RICH.
SQ SEQUENCE 1105 AA; 122869 MW; 586B818CE4FB5AEE CRC64;

Query Match 7.4%; Score 94; DB 1; Length 1105;
Best Local Similarity 21.2%; Pred. No. 3.1;
Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCNLNSALQVGCGAFACL 60
:||: :|:: | :||: | | :|| || :| : :
Db 308 LLQSRNAAVVMAVAQLYWH-----ISPKSE--AGVISKSLVRLRSNREVQYIVLQNI 358

Qy 61 ENSTCDTDGMYD-ICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFL----- 109
: : ||:: ||||| : | | | || :|| |
Db 359 ATMSIERKGMFEPYLKSF-YVRSTDPTMIKTLKLEILTNLANEANISTLLREFQTYVRSQ 417

Qy 110 -----AIRRCSTFQRMIAEVQEECYSKLNVCASIARKRNPEAITE---VVQLPNHFS 156
| ||:| |::| | || ::| || :| :| |::|
Db 418 DKQFAAATIQTIGRCAT---SISEFTETCFNGI-VCLLSNRDEIVVAESVVVIKKLLQMQ 473

Qy 157 NRYYNRLVRSLL-CDEDTVSTIRDLSMEKIGPNMASLFHILQTDHCAQTHPRADFNRR 215
: ::| :| | || | ||:: || | | | :| |
Db 474 PAQHGEIIRHMAKF LDSITVPVARASILWLIGEN-----CERVPKIA----- 515

Qy 216 TNEPQKLKVLLRNLRGED 234
| |:| :| :|
Db 516 ---PDVLRKMAKSFTSEDD 531

RESULT 15
SNAA_VITVI
ID SNAA_VITVI STANDARD; PRT; 289 AA.
AC P93798;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-soluble NSF attachment protein (Alpha-SNAP) (N-ethylmaleimide-

DE sensitive factor attachment protein, alpha).
 OS *Vitis vinifera* (Grape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 OC Vitaceae; *Vitis*.
 OX NCBI TaxID=29760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Shiraz; TISSUE=Fruit;
 RX MEDLINE=98182598; PubMed=9522131;
 RA Matsumoto S., Dry I.B., Thomas M.;
 RT "Nucleotide sequence of grapevine (*Vitis vinifera*) cDNA similar to
 SNAP proteins.";
 RL DNA Seq. 8:109-112(1997).
 CC -!- FUNCTION: Required for vesicular transport between the endoplasmic
 CC reticulum and the Golgi apparatus (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic peripheral membrane protein (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the SNAP family.
 CC -----
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 CC -----
 DR EMBL; AB001375; BAA19246.1; -.
 DR PIR; T50776; T50776.
 DR InterPro; IPR000744; NSF_attach.
 DR InterPro; IPR008941; TPR-like.
 DR InterPro; IPR001440; TPR.
 DR Pfam; PF02071; NSF; 4.
 DR PRINTS; PR00448; NSFATTACHMNT.
 KW Transport; Protein transport; Endoplasmic reticulum; Golgi stack.
 SQ SEQUENCE 289 AA; 32485 MW; 939E49A56C1388D4 CRC64;

Query Match 7.1%; Score 90.5; DB 1; Length 289;
 Best Local Similarity 19.9%; Pred. No. 1.2;
 Matches 41; Conservative 33; Mismatches 95; Indels 37; Gaps 5;

Qy	8 LLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACLENSTCDT 67
	:: : : : : : : : : : :
Db	59 LSTVIQSSDSKHEAAQ--AYADAGHCYKKTSAKEAISCLEQA-----AYLFLDNGRFNM 110
Qy	68 DG-----MYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQR 119
	: :: : : : : : : : : :
Db	111 AGKYYKEIAELYELEQNFEQAIYFEKAADIYQSEEATTAANQCNAKVAQFAAQLEQYQK 170
Qy	120 MIAEVQEECYSKLN-----VCSIAKRNPEAITEVVQL----PNHFSNR 158
	:: : : : : : :
Db	171 AIQIYEDIGRPSLNNNLLKYGVKGHLLNAGICQLCKGDVVAITNALDRYQEMDPTFSGTR 230
Qy	159 YYNRLVRSLLCEDDETVSTIRDSLME 184
	: ::
Db	231 EYKLLVDLAAADEVVKFTDAVKE 256

Search completed: July 19, 2004, 15:32:39
Job time : 15 secs